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ABSTRACT:

The present invention relates to single domain ligands derived from molecules in the immunoglobulin (Ig) superfamily, receptors comprising at least one such ligand, methods for cloning, amplifying and expressing DNA sequences encoding such ligands, preferably using the polymerase chain reaction, methods for the use of said DNA sequences in the production of Ig-type molecules and said ligands or receptors, and the use of said ligands or receptors in therapy, diagnosis or catalysis.

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(54) **Single domain ligands, receptors comprising said ligands, methods for their production, and use of said ligands and receptors.**

(57) The present invention relates to single domain ligands derived from molecules in the immunoglobulin (Ig) superfamily, receptors comprising at least one such ligand, methods for cloning, amplifying and expressing DNA sequences encoding such ligands, preferably using the polymerase chain reaction, methods for the use of said DNA sequences in the production of Ig-type molecules and said ligands or receptors; and the use of said ligands or receptors in therapy, diagnosis or catalysis.

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Single Domain Ligands, Receptors comprising said Ligands, Methods for their Production, and Use of said Ligands and Receptors

The present invention relates to single domain ligands derived from molecules in the immunoglobulin (Ig) superfamily, receptors comprising at least one such ligand, methods for cloning, amplifying and expressing DNA sequences encoding such ligands, methods for the use of said DNA sequences in the production of Ig-type molecules and said ligands or receptors, and the use of said ligands or receptors in therapy, diagnosis or catalysis.

A list of references is appended to the end of the description. The documents listed therein are referred to in the description by number, which is given in square brackets [].

The Ig superfamily includes not only the Igs themselves but also such molecules as receptors on lymphoid cells such as T lymphocytes. Immunoglobulins comprise at least one heavy and one light chain covalently bonded together. Each chain is divided into a number of domains. At the N terminal end of each chain is a variable domain. The variable domains on the heavy and light chains fit together to form a binding site designed to receive a particular target molecule. In the case of Igs, the target molecules are antigens. T-cell receptors have two chains of equal size, the α and β chains, each consisting of two domains. At the N-terminal end of each chain is a variable domain and the variable domains on the α and β chains are believed to fit together to form a binding site for target molecules, in this case peptides presented by a histocompatibility antigen. The variable domains are so called because their amino acid sequences vary particularly from one molecule to another. This variation in sequence enables the molecules to recognise an extremely wide variety of target molecules.

Much research has been carried out on Ig molecules to determine how the variable domains are produced. It has been shown that each variable domain comprises a number of areas of relatively conserved sequence and three areas of hypervariable sequence. The three hypervariable areas are generally known as complementarity determining regions (CDRs).

Crystallographic studies have shown that in each variable domain of an Ig molecule the CDRs are supported on framework areas formed by the arrays of conserved sequences. The three CDRs are brought together by the framework areas and, together with the CDRs on the other chain, form a pocket in which the target molecule is received.

Since the advent of recombinant DNA technology, there has been much interest in the use of

such technology to clone and express Ig molecules and derivatives thereof. This interest is reflected in the numbers of patent applications and other publications on the subject.

The earliest work on the cloning and expression of full Igs in the patent literature is EP-A-0 120 694 (Boss). The Boss application also relates to the cloning and expression of chimeric antibodies. Chimeric antibodies are Ig-type molecules in which the variable domains from one Ig are fused to constant domains from another Ig. Usually, the variable domains are derived from an Ig from one species (often a mouse Ig) and the constant domains are derived from an Ig from a different species (often a human Ig).

A later European patent application, EP-A-0 125 023 (Genentech), relates to much the same subject as the Boss application, but also relates to the production by recombinant DNA technology of other variations of Ig-type molecules.

EP-A-0 194 276 (Neuberger) discloses not only chimeric antibodies of the type disclosed in the Boss application but also chimeric antibodies in which some or all of the constant domains have been replaced by non-Ig derived protein sequences. For instance, the heavy chain CH2 and CH3 domains may be replaced by protein sequences derived from an enzyme or a protein toxin.

EP-A-0 239 400 (Winter) discloses a different approach to the production of Ig molecules. In this approach, only the CDRs from a first type of Ig are grafted onto a second type of Ig in place of its normal CDRs. The Ig molecule thus produced is predominantly of the second type, since the CDRs form a relatively small part of the whole Ig. However, since the CDRs are the parts which define the specificity of the Ig, the Ig molecule thus produced has its specificity derived from the first Ig.

Hereinafter, chimeric antibodies, CDR-grafted Igs, the altered antibodies described by Genentech, and fragments, of such Igs such as $F(ab')_2$ and Fv fragments are referred to herein as modified antibodies.

One of the main reasons for all the activity in the Ig field using recombinant DNA technology is the desire to use Igs in therapy. It is well known that, using the hybridoma technique developed by Kohler and Milstein, it is possible to produce monoclonal antibodies (MAbs) of almost any specificity. Thus, MAbs directed against cancer antigens have been produced. It is envisaged that these MAbs could be covalently attached or fused to toxins to provide "magic bullets" for use in cancer therapy.

MAbs directed against normal tissue or cell surface antigens have also been produced. Labels can be attached to these so that they can be used for *in vivo* imaging.

The major obstacle to the use of such MAbs in therapy or *in vivo* diagnosis is that the vast majority of MAbs which are produced are of rodent, in particular mouse, origin. It is very difficult to produce human MAbs. Since most MAbs are derived from non-human species, they are antigenic in humans. Thus, administration of these MAbs to humans generally results in an anti-Ig response being mounted by the human. Such a response can interfere with therapy or diagnosis, for instance by destroying or clearing the antibody quickly, or can cause allergic reactions or immune complex hypersensitivity which has adverse effects on the patient.

The production of modified Igs has been proposed to ensure that the Ig administered to a patient is as "human" as possible, but still retains the appropriate specificity. It is therefore expected that modified Igs will be as effective as the MAb from which the specificity is derived but at the same time not very antigenic. Thus, it should be possible to use the modified Ig a reasonable number of times in a treatment or diagnosis regime.

At the level of the gene, it is known that heavy chain variable domains are encoded by a "rearranged" gene which is built from three gene segments: an "unrearranged" VH gene (encoding the N-terminal three framework regions, first two complete CDRs and the first part of the third CDR), a diversity (DH)-segment (DH) (encoding the central portion of the third CDR) and a joining segment (JH) (encoding the last part of the third CDR and the fourth framework region). In the maturation of B-cells, the genes rearrange so that each unrearranged VH gene is linked to one DH gene and one JH gene. The rearranged gene corresponds to VH-DH-JH. This rearranged gene is linked to a gene which encodes the constant portion of the Ig chain.

For light chains, the situation is similar, except that for light chains there is no diversity region. Thus light chain variable domains are encoded by an "unrearranged" VL gene and a JL gene. There are two types of light chains, kappa (κ) or lambda (λ), which are built respectively from unrearranged V κ genes and J κ segments, and from unrearranged V λ genes and J λ segments.

Previous work has shown that it is necessary to have two variable domains in association together for efficient binding. For example, the associated heavy and light chain variable domains were shown to contain the antigen binding site [1]. This assumption is borne out by X-ray crystallographic studies of crystallised antibody/antigen complexes [2-6] which show that both the heavy and light chains of the antibody's variable domains contact

the antigen. The expectation that association of heavy and light chain variable domains is necessary for efficient antigen binding underlies work to co-ordinate these domains from bacteria [1], and to link the domains together by a short section of polypeptide as in the single chain antibodies [8, 9].

Binding of isolated heavy and light chains had also been detected. However the evidence suggested strongly that this was a property of heavy or light chain dimers. Early work, mainly with polyclonal antibodies, in which antibody heavy and light chains had been separated under denaturing conditions [10] suggested that isolated antibody heavy chains could bind to protein antigens [11] or haptens [12]. The binding of protein antigen was not characterised, but the hapten-binding affinity of the heavy chain fragments was reduced by two orders of magnitude [12] and the number of hapten molecules binding were variously estimated as 0.14 or 0.37 [13] or 0.26 [14] per isolated heavy chain. Furthermore binding of haptens was shown to be a property of dimeric heavy or dimeric light chains [14]. Indeed light chain dimers have been crystallised. It has been shown that in light chain dimers the two chains form a cavity which is able to bind to a single molecule of hapten [15].

This confirms the assumption that, in order to obtain efficient binding, it is necessary to have a dimer, and preferably a heavy chain/light chain dimer, containing the respective variable domains. This assumption also underlies the teaching of the patent references cited above, wherein the intention is always to produce dimeric, and preferably heavy/light chain dimeric, molecules.

It has now been discovered, contrary to expectations, that isolated Ig heavy chain variable domains can bind to antigen in a 1:1 ratio and with binding constants of equivalent magnitude to those of complete antibody molecules. In view of what was known up until now and in view of the assumptions made by those skilled in the art, this is highly surprising.

Therefore, according to a first aspect of the present invention, there is provided a single domain ligand consisting at least part of the variable domain of one chain of a molecule from the Ig superfamily.

Preferably, the ligand consists of the variable domain of an Ig light, or, most preferably, heavy chain.

The ligand may be produced by any known technique, for instance by controlled cleavage of Ig superfamily molecules or by peptide synthesis. However, preferably the ligand is produced by recombinant DNA technology. For instance, the gene encoding the rearranged gene for a heavy chain variable domain may be produced, for instance by cloning or gene synthesis, and placed into a suit-

able expression vector. The expression vector is then used to transform a compatible host cell which is then cultured to allow the ligand to be expressed and, preferably, secreted.

If desired, the gene for the ligand can be mutated to improve the properties of the expressed domain, for example to increase the yields of expression or the solubility of the ligand, to enable the ligand to bind better, or to introduce a second site for covalent attachment (by introducing chemically reactive residues such as cysteine and histidine) or non-covalent binding of other molecules. In particular it would be desirable to introduce a second site for binding to serum components, to prolong the residence time of the domains in the serum; or for binding to molecules with effector functions, such as components of complement, or receptors on the surfaces of cells.

Thus, hydrophobic residues which would normally be at the interface of the heavy chain variable domain with the light chain variable domain could be mutated to more hydrophilic residues to improve solubility; residues in the CDR loops could be mutated to improve antigen binding; residues on the other loops or parts of the β -sheet could be mutated to introduce new binding activities. Mutations could include single point mutations, multiple point mutations or more extensive changes and could be introduced by any of a variety of recombinant DNA methods, for example gene synthesis, site directed mutagenesis or the polymerase chain reaction.

Since the ligands of the present invention have equivalent binding affinity to that of complete Ig molecules, the ligands can be used in many of the ways as are Ig molecules or fragments. For example, Ig molecules have been used in therapy (such as in treating cancer, bacterial and viral diseases), in diagnosis (such as pregnancy testing), in vaccination (such as in producing anti-idiotypic antibodies which mimic antigens), in modulation of activities of hormones or growth factors, in detection, in biosensors and in catalysis.

It is envisaged that the small size of the ligands of the present invention may confer some advantages over complete antibodies, for example, in neutralising the activity of low molecular weight drugs (such as digoxin) and allowing their filtration from the kidneys with drug attached; in penetrating tissues and tumours; in neutralising viruses by binding to small conserved regions on the surfaces of viruses such as the "canyon" sites of viruses [16]; in high resolution epitope mapping of proteins; and in vaccination by ligands which mimic antigens.

The present invention also provides receptors comprising a ligand according to the first aspect of the invention linked to one or more of an effector

molecule, a label, a surface, or on one or more other ligands having the same or different specificity.

A receptor comprising a ligand linked to an effector molecule may be of use in therapy. The effector molecule may be a toxin, such as ricin or pseudomonas exotoxin, an enzyme which is able to activate a prodrug, a binding partner or a radio-isotope. The radio-isotope may be directly linked to the ligand or may be attached thereto by a chelating structure which is directly linked to the ligand. Such ligands with attached isotopes are much smaller than those based on Fv fragments, and could penetrate tissues and access tumours more readily.

A receptor comprising a ligand linked to a label may be of use in diagnosis. The label may be a heavy metal atom or a radio-isotope, in which case the receptor can be used for *in vivo* imaging using X-ray or other scanning apparatus. The metal atom or radio-isotope may be attached to the ligand either directly or via a chelating structure directly linked to the ligand. For *in vitro* diagnostic testing, the label may be a heavy metal atom, a radio-isotope, an enzyme, a fluorescent or coloured molecule or a protein or peptide tag which can be detected by an antibody, an antibody fragment or another protein. Such receptors would be used in any of the known diagnostic tests, such as ELISA or fluorescence-linked assays.

A receptor comprising a ligand linked to a surface, such as a chromatography medium, could be used for purification of other molecules by affinity chromatography. Linking of ligands to cells, for example to the outer membrane proteins of *E. coli* or to hydrophobic tails which localise the ligands in the cell membranes, could allow a simple diagnostic test in which the bacteria or cells would agglutinate in the presence of molecules bearing multiple sites for binding the ligand(s).

Receptors comprising at least two ligands can be used, for instance, in diagnostic tests. The first ligand will bind to a test antigen and the second ligand will bind to a reporter molecule, such as an enzyme, a fluorescent dye, a coloured dye, a radio-isotope or a coloured-, fluorescently- or radio-labelled protein.

Alternatively, such receptors may be useful in increasing the binding to an antigen. The first ligand will bind to a first epitope of the antigen and the second ligand will bind to a second epitope. Such receptors may also be used for increasing the affinity and specificity of binding to different antigens in close proximity on the surface of cells. The first ligand will bind to the first antigen and the second epitope to the second antigen: strong binding will depend on the co-expression of the epitopes on the surface of the cell. This may be useful in therapy of tumours, which can have elevated

expression of several surface markers. Further ligands could be added to further improve binding or specificity. Moreover, the use of strings of ligands, with the same or multiple specificities, creates a larger molecule which is less readily filtered from the circulation by the kidney.

For vaccination with ligands which mimic antigens, the use of strings of ligands may prove more effective than single ligands, due to repetition of the immunising epitopes.

If desired, such receptors with multiple ligands could include effector molecules or labels so that they can be used in therapy or diagnosis as described above.

The ligand may be linked to the other part of the receptor by any suitable means, for instance by covalent or non-covalent chemical linkages. However, where the receptor comprises a ligand and another protein molecule, it is preferred that they are produced by recombinant DNA technology as a fusion product. If necessary, a linker peptide sequence can be placed between the ligand and the other protein molecule to provide flexibility.

The basic techniques for manipulating Ig molecules by recombinant DNA technology are described in the patent references cited above. These may be adapted in order to allow for the production of ligands and receptors according to the invention by means of recombinant DNA technology.

Preferably, where the ligand is to be used for *in vivo* diagnosis or therapy in humans, it is humanised, for instance by CDR replacement as described in EP-A-0 239 400.

In order to obtain a DNA sequence encoding a ligand, it is generally necessary firstly to produce a hybridoma which secretes an appropriate MAb. This can be a very time consuming method. Once an immunised animal has been produced, it is necessary to fuse separated spleen cells with a suitable myeloma cell line, grow up the cell lines thus produced, select appropriate lines, reclone the selected lines and reselect. This can take some long time. This problem also applies to the production of modified Igs.

A further problem with the production of ligands, and also receptors according to the invention and modified Igs, by recombinant DNA technology is the cloning of the variable domain encoding sequences from the hybridoma which produces the MAb from which the specificity is to be derived. This can be a relatively long method involving the production of a suitable probe, construction of a clone library from cDNA or genomic DNA, extensive probing of the clone library, and manipulation of any isolated clones to enable the cloning into a suitable expression vector. Due to the inherent variability of the DNA sequences encoding Ig variable domains, it has not previously been possible

to avoid such time consuming work. It is therefore a further aim of the present invention to provide a method which enables substantially any sequence encoding an Ig superfamily molecule variable domain (ligand) to be cloned in a reasonable period of time.

According to another aspect of the present invention therefore, there is provided a method of cloning a sequence (the target sequence) which encodes at least part of the variable domain of an Ig superfamily molecule, which method comprises:

(a) providing a sample of double stranded (ds) nucleic acid which contains the target sequence;

(b) denaturing the sample so as to separate the two strands;

(c) annealing to the sample a forward and a back oligonucleotide primer, the forward primer being specific for a sequence at or adjacent the 3' end of the sense strand of the target sequence, the back primer being specific for a sequence at or adjacent the 3' end of the antisense strand of the target sequence, under conditions which allow the primers to hybridise to the nucleic acid at or adjacent the target sequence;

(d) treating the annealed sample with a DNA polymerase enzyme in the presence of deoxynucleoside triphosphates under conditions which cause primer extension to take place; and

(e) denaturing the sample under conditions such that the extended primers become separated from the target sequence.

Preferably, the method of the present invention further includes the step (f) of repeating steps (c) to (e) on the denatured mixture a plurality of times.

Preferably, the method of the present invention is used to clone complete variable domains from Ig molecules, most preferably from Ig heavy chains. In the most preferred instance, the method will produce a DNA sequence encoding a ligand according to the present invention.

In step (c) recited above, the forward primer becomes annealed to the sense strand of the target sequence at or adjacent the 3' end of the strand. In a similar manner, the back primer becomes annealed to the antisense strand of the target sequence at or adjacent the 3' end of the strand. Thus, the forward primer anneals at or adjacent the region of the ds nucleic acid which encodes the C terminal end of the variable region or domain. Similarly, the back primer anneals at or adjacent the region of the ds nucleic acid which encodes the N-terminal end of the variable domain.

In step (d), nucleotides are added onto the 3' end of the forward and back primers in accordance with the sequence of the strand to which they are annealed. Primer extension will continue in this manner until stopped by the beginning of the de-

naturing step (e). It must therefore be ensured that step (d) is carried out for a long enough time to ensure that the primers are extended so that the extended strands totally overlap on another.

In step (e), the extended primers are separated from the ds nucleic acid. The ds nucleic acid can then serve again as a substrate to which further primers can anneal. Moreover, the extended primers themselves have the necessary complementary sequences to enable the primers to anneal thereto.

During further cycles, if step (f) is used, the amount of extended primers will increase exponentially so that at the end of the cycles there will be a large quantity of cDNA having sequences complementary to the sense and antisense strands of the target sequence. Thus, the method of the present invention will result in the accumulation of a large quantity of cDNA which can form ds cDNA encoding at least part of the variable domain.

As will be apparent to the skilled person, some of the steps in the method may be carried out simultaneously or sequentially as desired.

The forward and back primers may be provided as isolated oligonucleotides, in which case only two oligonucleotides will be used. However, alternatively the forward and back primers may each be supplied as a mixture of closely related oligonucleotides. For instance, it may be found that at a particular point in the sequence to which the primer is to anneal, there is the possibility of nucleotide variation. In this case a primer may be used for each possible nucleotide variation. Furthermore it may be possible to use two or more sets of "nested" primers in the method to enhance the specific cloning of variable region genes.

The method described above is similar to the method described by Saiki et al. [17]. A similar method is also used in the methods described in EP-A-0 200 362. In both cases the method described is carried out using primers which are known to anneal efficiently to the specified nucleotide sequence. In neither of these disclosures was it suggested that the method could be used to clone Ig parts of variable domain encoding sequences, where the target sequence contains inherently highly variable areas.

The ds nucleic acid sequence used in the method of the present invention may be derived from mRNA. For instance, RNA may be isolated in known manner from a cell or cell line which is known to produce Igs. mRNA may be separated from other RNA by oligo-dT chromatography. A complementary strand of cDNA may then be synthesised on the mRNA template, using reverse transcriptase and a suitable primer, to yield an RNA/DNA heteroduplex. A second strand of DNA can be made in one of several ways, for example, by priming with RNA fragments of the mRNA

strand (made by incubating RNA/DNA heteroduplex with RNase H) and using DNA polymerase, or by priming with a synthetic oligodeoxynucleotide primer which anneals to the 3' end of the first strand and using DNA polymerase. It has been found that the method of the present invention can be carried out using ds cDNA prepared in this way.

When making such ds cDNA, it is possible to use a forward primer which anneals to a sequence in the CH1 domain (for a heavy chain variable domain) or the C λ or C κ domain (for a light chain variable domain). These will be located in close enough proximity to the target sequence to allow the sequence to be cloned.

The back primer may be one which anneals to a sequence at the N-terminal end of the VH1, V κ or V λ domain. The back primer may consist of a plurality of primers having a variety of sequences designed to be complementary to the various families of VH1, V κ or V λ sequences known. Alternatively the back primer may be a single primer having a consensus sequence derived from all the families of variable region genes.

Surprisingly, it has been found that the method of the present invention can be carried out using genomic DNA. If genomic DNA is used, there is a very large amount of DNA present, including actual coding sequences, introns and untranslated sequences between genes. Thus, there is considerable scope for non-specific annealing under the conditions used. However, it has surprisingly been found that there is very little non-specific annealing. It is therefore unexpected that it has proved possible to clone the genes of Ig-variable domains from genomic DNA.

Under some circumstances the use of genomic DNA may prove advantageous compared with use of mRNA, as the mRNA is readily degraded, and especially difficult to prepare from clinical samples of human tissue.

Thus, in accordance with an aspect of the present invention, the ds nucleic acid used in step (a) is genomic DNA.

When using genomic DNA as the ds nucleic acid source, it will not be possible to use as the forward primer an oligonucleotide having a sequence complementary to a sequence in a constant domain. This is because, in genomic DNA, the constant domain genes are generally separated from the variable domain genes by a considerable number of base pairs. Thus, the site of annealing would be too remote from the sequence to be cloned.

It should be noted that the method of the present invention can be used to clone both rearranged and unrearranged variable domain sequences from genomic DNA. It is known that in germ line genomic DNA the three genes, encoding

the VH, DH and JH respectively, are separated from one another by considerable numbers of base pairs. On maturation of the immune response, these genes are rearranged so that the VH, DH and JH genes are fused together to provide the gene encoding the whole variable domain (see Figure 1). By using a forward primer specific for a sequence at or adjacent the 3' end of the sense strand of the genomic "unrearranged" VH gene, it is possible to clone the "unrearranged" VH gene alone, without also cloning the DH and JH genes. This can be of use in that it will then be possible to fuse the VH gene onto pre-cloned or synthetic DH and JH genes. In this way, rearrangement of the variable domain genes can be carried out *in vitro*.

The oligonucleotide primers used in step (c) may be specifically designed for use with a particular target sequence. In this case, it will be necessary to sequence at least the 5' and 3' ends of the target sequence so that the appropriate oligonucleotides can be synthesised. However, the present inventors have discovered that it is not necessary to use such specifically designed primers. Instead, it is possible to use a species specific general primer or a mixture of such primers for annealing to each end of the target sequence. This is not particularly surprising as regards the 3' end of the target sequence. It is known that this end of the variable domain encoding sequence leads into a segment encoding JH which is known to be relatively conserved. However, it was surprisingly discovered that, within a single species, the sequence at the 5' end of the target sequence is sufficiently well conserved to enable a species specific general primer or a mixture thereof to be designed for the 5' end of the target sequence.

Therefore according to a preferred aspect of the present invention, in step (c) the two primers which are used are species specific general primers, whether used as single primers or as mixtures of primers. This greatly facilitates the cloning of any undetermined target sequence since it will avoid the need to carry out any sequencing on the target sequence in order to produce target sequence-specific primers. Thus the method of this aspect of the invention provides a general method for cloning variable region or domain encoding sequences of a particular species.

Once the variable domain gene has been cloned using the method described above, it may be directly inserted into an expression vector, for instance using the PCR reaction to paste the gene into a vector.

Advantageously, however, each primer includes a sequence including a restriction enzyme recognition site. The sequence recognised by the restriction enzyme need not be in the part of the primer which anneals to the ds nucleic acid, but

may be provided as an extension which does not anneal. The use of primers with restriction sites has the advantage that the DNA can be cut with at least one restriction enzyme which leaves 3' or 5' overhanging nucleotides. Such DNA is more readily cloned into the corresponding sites on the vectors than blunt end fragments taken directly from the method. The ds cDNA produced at the end of the cycles will thus be readily insertable into a cloning vector by use of the appropriate restriction enzymes. Preferably the choice of restriction sites is such that the ds cDNA is cloned directly into an expression vector, such that the ligand encoded by the gene is expressed. In this case the restriction site is preferably located in the sequence which is annealed to the ds nucleic acid.

Since the primers may not have a sequence exactly complementary to the target sequence to which it is to be annealed, for instance because of nucleotide variations or because of the introduction of a restriction enzyme recognition site, it may be necessary to adjust the conditions in the annealing mixture to enable the primers to anneal to the ds nucleic acid. This is well within the competence of the person skilled in the art and needs no further explanation.

In step (d), any DNA polymerase may be used. Such polymerases are known in the art and are available commercially. The conditions to be used with each polymerase are well known and require no further explanation here. The polymerase reaction will need to be carried out in the presence of the four nucleoside triphosphates. These and the polymerase enzyme may already be present in the sample or may be provided afresh for each cycle.

The denaturing step (e) may be carried out, for instance, by heating the sample, by use of chaotropic agents, such as urea or guanidine, or by the use of changes in ionic strength or pH. Preferably, denaturing is carried out by heating since this is readily reversible. Where heating is used to carry out the denaturing, it will be usual to use a thermostable DNA polymerase, such as Taq polymerase, since this will not need replenishing at each cycle.

If heating is used to control the method, a suitable cycle of heating comprises denaturation at about 95°C for about 1 minute, annealing at from 30°C to 65°C for about 1 minute and primer extension at about 75°C for about 2 minutes. To ensure that elongation and renaturation is complete, the mixture after the final cycle is preferably held at about 60°C for about 5 minutes.

The product ds cDNA may be separated from the mixture for instance by gel electrophoresis using agarose gels. However, if desired, the ds cDNA may be used in unpurified form and inserted directly into a suitable cloning or expression vector

by conventional methods. This will be particularly easy to accomplish if the primers include restriction enzyme recognition sequences.

The method of the present invention may be used to make variations in the sequences encoding the variable domains. For example this may be achieved by using a mixture of related oligonucleotide primers as at least one of the primers. Preferably the primers are particularly variable in the middle of the primer and relatively conserved at the 5' and 3' ends. Preferably the ends of the primers are complementary to the framework regions of the variable domain, and the variable region in the middle of the primer covers all or part of a CDR. Preferably a forward primer is used in the area which forms the third CDR. If the method is carried out using such a mixture of oligonucleotides, the product will be a mixture of variable domain encoding sequences. Moreover, variations in the sequence may be introduced by incorporating some mutagenic nucleotide triphosphates in step (d), such that point mutations are scattered throughout the target region. Alternatively such point mutations are introduced by performing a large number of cycles of amplification, as errors due to the natural error rate of the DNA polymerase are amplified, particularly when using high concentrations of nucleoside triphosphates.

The method of this aspect of the present invention has the advantage that it greatly facilitates the cloning of variable domain encoding sequences directly from mRNA or genomic DNA. This in turn will facilitate the production of modified Ig-type molecules by any of the prior art methods referred to above. Further, target genes can be cloned from tissue samples containing antibody producing cells, and the genes can be sequenced. By doing this, it will be possible to look directly at the immune repertoire of a patient. This "fingerprinting" of a patient's immune repertoire could be of use in diagnosis, for instance of autoimmune diseases.

In the method for amplifying the amount of a gene encoding a variable domain, a single set of primers is used in several cycles of copying via the polymerase chain reaction. As a less preferred alternative, there is provided a second method which comprises steps (a) to (d) as above, which further includes the steps of:

(g) treating the sample of ds cDNA with traces of DNase in the presence of DNA polymerase I to allow nick translation of the DNA; and

(h) cloning the ds cDNA into a vector.

If desired, the second method may further include the steps of:

(i) digesting the DNA of recombinant plasmids to release DNA fragments containing genes

encoding variable domains; and

(j) treating the fragments in a further set of steps (c) to (h).

Preferably the fragments are separated from the vector and from other fragments of the incorrect size by gel electrophoresis.

The steps (a) to (d) then (g) to (h) can be followed once, but preferably the entire cycle (c) to (d) and (g) to (j) is repeated at least once. In this way a priming step, in which the genes are specifically copied, is followed by a cloning step, in which the amount of genes is increased.

In step (a) the ds cDNA is derived from mRNA. For Ig derived variable domains, the mRNA is preferably be isolated from lymphocytes which have been stimulated to enhance production of mRNA.

In each step (c) the set of primers are preferably different from the previous step (c), so as to enhance the specificity of copying. Thus the sets of primers form a nested set. For example, for cloning of Ig heavy chain variable domains, the first set of primers may be located within the signal sequence and constant region, as described by Larrick et al., [18], and the second set of primers entirely within the variable region, as described by Orlandi et al., [19]. Preferably the primers of step (c) include restriction sites to facilitate subsequent cloning. In the last cycle the set of primers used in step (c) should preferably include restriction sites for introduction into expression vectors. In step (g) possible mismatches between the primers and the template strands are corrected by "nick translation". In step (h), the ds cDNA is preferably cleaved with restriction enzymes at sites introduced into the primers to facilitate the cloning.

According to another aspect of the present invention the product ds cDNA is cloned directly into an expression vector. The host may be prokaryotic or eukaryotic, but is preferably bacterial. Preferably the choice of restriction sites in the primers and in the vector, and other features of the vector will allow the expression of complete ligands, while preserving all those features of the amino acid sequence which are typical of the (methoded) ligands. For example, for expression of the rearranged variable genes, the primers would be chosen to allow the cloning of target sequences including at least all the three CDR sequences. The cloning vector would then encode a signal sequence (for secretion of the ligand), and sequences encoding the N-terminal end of the first framework region, restriction sites for cloning and then the C-terminal end of the last (fourth) framework region.

For expression of unrearranged VH genes as part of complete ligands, the primers would be chosen to allow the cloning of target sequences including at least the first two CDRs. The cloning

vector could then encode signal sequence, the N-terminal end of the first framework region, restriction sites for cloning and then the C-terminal end of the third framework region, the third CDR and fourth framework region.

Primers and cloning vectors may likewise be devised for expression of single CDRs, particularly the third CDR, as parts of complete ligands. The advantage of cloning repertoires of single CDRs would permit the design of a "universal" set of framework regions, incorporating desirable properties such as solubility.

Single ligands could be expressed alone or in combination with a complementary variable domain. For example, a heavy chain variable domain can be expressed either as an individual domain or, if it is expressed with a complementary light chain variable domain, as an antigen binding site. Preferably the two partners would be expressed in the same cell, or secreted from the same cell, and the proteins allowed to associate non-covalently to form an Fv fragment. Thus the two genes encoding the complementary partners can be placed in tandem and expressed from a single vector, the vector including two sets of restriction sites.

Preferably the genes are introduced sequentially: for example the heavy chain variable domain can be cloned first and then the light chain variable domain. Alternatively the two genes are introduced into the vector in a single step, for example by using the polymerase chain reaction to paste together each gene with any necessary intervening sequence, as essentially described by Yon and Fried [29]. The two partners could be also expressed as a linked protein to produce a single chain Fv fragment, using similar vectors to those described above. As a further alternative the two genes may be placed in two different vectors, for example in which one vector is a phage vector and the other is a plasmid vector.

Moreover, the cloned ds cDNA may be inserted into an expression vector already containing sequences encoding one or more constant domains to allow the vector to express Ig-type chains. The expression of Fab fragments, for example, would have the advantage over Fv fragments that the heavy and light chains would tend to associate through the constant domains in addition to the variable domains. The final expression product may be any of the modified Ig-type molecules referred to above.

The cloned sequence may also be inserted into an expression vector so that it can be expressed as a fusion protein. The variable domain encoding sequence may be linked directly or via a linker sequence to a DNA sequence encoding any protein effector molecule, such as a toxin, enzyme, label or another ligand. The variable domain se-

quences may also be linked to proteins on the outer side of bacteria or phage. Thus, the method of this aspect of the invention may be used to produce receptors according to the invention.

According to another aspect of the invention, the cloning of ds cDNA directly for expression permits the rapid construction of expression libraries which can be screened for binding activities. For Ig heavy and light chain variable genes, the ds cDNA may comprise variable genes isolated as complete rearranged genes from the animal, or variable genes built from several different sources, for example a repertoire of unrearranged VH genes combined with a synthetic repertoire of DH and JH genes. Preferably repertoires of genes encoding Ig heavy chain variable domains are prepared from lymphocytes of animals immunised with an antigen.

The screening method may take a range of formats well known in the art. For example Ig heavy chain variable domains secreted from bacteria may be screened by binding to antigen on a solid phase, and detecting the captured domains by antibodies. Thus the domains may be screened by growing the bacteria in liquid culture and binding to antigen coated on the surface of ELISA plates. However, preferably bacterial colonies (or phage plaques) which secrete ligands (or modified ligands, or ligand fusions with proteins) are screened for antigen binding on membranes. Either the ligands are bound directly to the membranes (and for example detected with labelled antigen), or captured on antigen coated membranes (and detected with reagents specific for ligands). The use of membranes offers great convenience in screening many clones, and such techniques are well known in the art.

The screening method may also be greatly facilitated by making protein fusions with the ligands, for example by introducing a peptide tag which is recognised by an antibody at the N-terminal or C-terminal end of the ligand, or joining the ligand to an enzyme which catalyses the conversion of a colourless substrate to a coloured product. In the latter case, the binding of antigen may be detected simply by adding substrate. Alternatively, for ligands expressed and folded correctly inside eukaryotic cells, joining of the ligand and a domain of a transcriptional activator such as the GAL4 protein of yeast, and joining of antigen to the other domain of the GAL4 protein, could form the basis for screening binding activities, as described by Fields and Song [21].

The preparation of proteins, or even cells with multiple copies of the ligands, may improve the avidity of the ligand for immobilised antigen, and hence the sensitivity of the screening method. For example, the ligand may be joined to a protein

subunit of a multimeric protein, to a phage coat protein or to an outer membrane protein of *E. coli* such as ompA or lamB. Such fusions to phage or bacterial proteins also offers possibilities of selecting bacteria displaying ligands with antigen binding activities. For example such bacteria may be precipitated with antigen bound to a solid support, or may be subjected to affinity chromatography, or may be bound to larger cells or particles which have been coated with antigen and sorted using a fluorescence activated cell sorter (FACS). The proteins or peptides fused to the ligands are preferably encoded by the vector, such that cloning of the ds cDNA repertoire creates the fusion product.

In addition to screening for binding activities of single ligands, it may be necessary to screen for binding or catalytic activities of associated ligands, for example, the associated Ig heavy and light chain variable domains. For example, repertoires of heavy and light chain variable genes may be cloned such that two domains are expressed together. Only some of the pairs of domains may associate, and only some of these associated pairs may bind to antigen. The repertoires of heavy and light chain variable domains could be cloned such that each domain is paired at random. This approach may be most suitable for isolation of associated domains in which the presence of both partners is required to form a cleft. Alternatively, to allow the binding of hapten. Alternatively, since the repertoires of light chain sequences are less diverse than those of heavy chains, a small repertoire of light chain variable domains, for example including representative members of each family of domains, may be combined with a large repertoire of heavy chain variable domains.

Preferably however, a repertoire of heavy chain variable domains is screened first for antigen binding in the absence of the light chain partner, and then only those heavy chain variable domains binding to antigen are combined with the repertoire of light chain variable domains. Binding of associated heavy and light chain variable domains may be distinguished readily from binding of single domains, for example by fusing each domain to a different C-terminal peptide tag which are specifically recognised by different monoclonal antibodies.

The hierarchical approach of first cloning heavy chain variable domains with binding activities, then cloning matching light chain variable domains may be particularly appropriate for the construction of catalytic antibodies, as the heavy chain may be screened first for substrate binding. A light chain variable domain would then be identified which is capable of association with the heavy chain, and "catalytic" residues such as cysteine or histidine (or prosthetic groups) would be introduced into the

CDRs to stabilise the transition state or attack the substrate, as described by Baldwin and Schultz [22].

Although the binding activities of non-covalently associated heavy and light chain variable domains (Fv fragments) may be screened, suitable fusion proteins may drive the association of the variable domain partners. Thus Fab fragments are more likely to be associated than the Fv fragments, as the heavy chain variable domain is attached to a single heavy chain constant domain, and the light chain variable domain is attached to a single light chain variable domain, and the two constant domains associate together.

Alternatively the heavy and light chain variable domains are covalently linked together with a peptide, as in the single chain antibodies, or peptide sequences attached, preferably at the C-terminal end which will associate through forming cysteine bonds or through non-covalent interactions, such as the introduction of "leucine zipper" motifs. However, in order to isolate pairs of tightly associated variable domains, the Fv fragments are preferably used.

The construction of Fv fragments isolated from a repertoire of variable region genes offers a way of building complete antibodies, and an alternative to hybridoma technology. For example by attaching the variable domains to light or suitable heavy chain constant domains, as appropriate, and expressing the assembled genes in mammalian cells, complete antibodies may be made and should possess natural effector functions, such as complement lysis. This route is particularly attractive for the construction of human monoclonal antibodies, as hybridoma technology has proved difficult, and for example, although human peripheral blood lymphocytes can be immortalised with Epstein Barr virus, such hybridomas tend to secrete low affinity IgM antibodies.

Moreover, it is known that immunological mechanisms ensure that lymphocytes do not generally secrete antibodies directed against host proteins. However it is desirable to make human antibodies directed against human proteins, for example to human cell surface markers to treat cancers, or to histocompatibility antigens to treat autoimmune diseases. The construction of human antibodies built from the combinatorial repertoire of heavy and light chain variable domains may overcome this problem, as it will allow human antibodies to be built with specificities which would normally have been eliminated.

The method also offers a new way of making bispecific antibodies. Antibodies with dual specificity can be made by fusing two hybridomas of different specificities, so as to make a hybrid antibody with an Fab arm of one specificity, and the

other Fab arm of a second specificity. However the yields of the bispecific antibody are low, as heavy and light chains also find the wrong partners. The construction of Fv fragments which are tightly associated should preferentially drive the association of the correct pairs of heavy with light chains. (It would not assist in the correct pairing of the two heavy chains with each other.) The improved production of bispecific antibodies would have a variety of applications in diagnosis and therapy, as is well known.

Thus the invention provides a species specific general oligonucleotide primer or a mixture of such primers useful for cloning variable domain encoding sequences from animals of that species. The method allows a single pair or pair of mixtures of species specific general primers to be used to clone any desired antibody specificity from that species. This eliminates the need to carry out any sequencing of the target sequence to be cloned and the need to design specific primers for each specificity to be recovered.

Furthermore it provides for the construction of repertoires of variable genes, for the expression of the variable genes directly on cloning, for the screening of the encoded domains for binding activities and for the assembly of the domains with other variable domains derived from the repertoire.

Thus the use of the method of the present invention will allow for the production of heavy chain variable domains with binding activities and variants of these domains. It allows for the production of monoclonal antibodies and bispecific antibodies, and will provide an alternative to hybridoma technology. For instance, mouse splenic ds mRNA or genomic DNA may be obtained from a hyperimmunised mouse. This could be cloned using the method of the present invention and then the cloned ds DNA inserted into a suitable expression vector. The expression vector would be used to transform a host cell, for instance a bacterial cell, to enable it to produce an Fv fragment or a Fab fragment. The Fv or Fab fragment would then be built into a monoclonal antibody by attaching constant domains and expressing it in mammalian cells.

The present invention is now described, by way of example only, with reference to the accompanying drawings in which:

Figure 1 shows a schematic representation of the unrearranged and rearranged heavy and light chain variable genes and the location of the primers;

Figure 2 shows a schematic representation of the M13-VHPCR1 vector and a cloning scheme for amplified heavy chain variable domains;

Figure 3 shows the sequence of the Ig variable region derived sequences in M13-VHPCR1;

Figure 4 shows a schematic representation of the M13-VKPCR1 vector and a cloning scheme for light chain variable domains;

Figure 5 shows the sequence of the Ig variable region derived sequences in M13-VKPCR1;

Figure 6 shows the nucleotide sequences of the heavy and light chain variable domain encoding sequences of MAb MBr1;

Figure 7 shows a schematic representation of the pSV-gpt vector (also known as α -Lys 30) which contains a variable region cloned as a HindIII-BamHI fragment, which is excised on introducing the new variable region. The gene for human IgG1 has also been engineered to remove a BamHI site, such that the BamHI site in the vector is unique;

Figure 8 shows a schematic representation of the pSV-hygro vector (also known as α -Lys 17). It is derived from pSV gpt vector with the gene encoding mycophenolic acid replaced by a gene coding for hygromycin resistance. The construct contains a variable gene cloned as a HindIII-BamHI fragment which is excised on introducing the new variable region. The gene for human C κ has also been engineered to remove a BamHI site, such that the BamHI site in the vector is unique;

Figure 9 shows the assembly of the mouse: human MBr1 chimaeric antibody;

Figure 10 shows encoded amino acid sequences of 48 mouse rearranged VH genes;

Figure 11 shows encoded amino acid sequences of human rearranged VH genes;

Figure 12 shows encoded amino acid sequences of unrearranged human VH genes;

Figure 13 shows the sequence of part of the plasmid pSW1: essentially the sequence of a pectate lyase leader linked to VHLYS in pSW1 and cloned as an SphI-EcoRI fragment into pUC19 and the translation of the open reading frame encoding the pectate lyase leader-VHLYS polypeptide being shown;

Figure 14 shows the sequence of part of the plasmid pSW2: essentially the sequence of a pectate lyase leader linked to VHLYS and to VKLYS, and cloned as an SphI-EcoRI-EcoRI fragment into pUC19 and the translation of open reading frames encoding the pectate lyase leader-VHLYS and pectate lyase leader-VKLYS polypeptides being shown;

Figure 15 shows the sequence of part of the plasmid pSW1HPOLYMYC which is based on pSW1 and in which a polylinker sequence has replaced the variable domain of VHLYS, and acts as a cloning site for amplified VH genes, and a peptide tag is introduced at the C-terminal end;

Figure 16 shows the encoded amino acid sequences of two VH domains derived from mouse spleen and having lysozyme binding activity, and compared with the VH domain of the D1,3 anti-

body. The arrows mark the points of difference between the two VH domains;

Figure 17 shows the encoded amino acid sequence of a VH domain derived from human peripheral blood lymphocytes and having lysozyme binding activity;

Figure 18 shows a scheme for generating and cloning mutants of the VHLYS gene, which is compared with the scheme for cloning natural repertoires of VH genes;

Figure 19 shows the sequence of part of the vector pSW2HPOLY;

Figure 20 shows the sequence of part of the vector pSW3 which encodes the two linked VHLYS domains;

Figure 21 shows the sequence of the VHLYS domain and pelB leader sequence fused to the alkaline phosphatase gene;

Figure 22 shows the sequence of the vector pSW1VHLYSVKPOLYMYC for expression of a repertoire of V_κ light chain variable domains in association with the VHLYS domain; and

Figure 23 shows the sequence of VH domain which is secreted at high levels from *E. coli*. The differences with VHLYS domain are marked.

PRIMERS

In the Examples described below, the following oligonucleotide primers, or mixed primers were used. Their locations are marked on Figure 1 and sequences are as follows:

VH1FOR 5' TGAGGAGACGGTGACCGTGGTCCC-
TTGGCCCCAG 3';
VH1FOR-2 5' TGAGGAGACGGT-
GACCGTGGTCCCTTGGCCCC 3';
Hu1VHFOR 5' CTTGGTGGAGGCTGAGGAGACG-
GTGACC 3';
Hu2VHFOR 5' CTTGGTGGAGGCTGAGGAGACG-
GTGACC 3';
Hu3VHFOR 5' CTTGGTGGATGCTGAGGAGACG-
GTGACC 3';
Hu4VHFOR 5' CTTGGTGGATGCTGATGAGACGG-
TGACC 3';
MOJH1FOR 5' TGAGGAGACGGTGACCGTGGTC-
CCTGCGCCCCAG 3';
MOJH2FOR 5' TGAGGAGACGGTGACCGTGGTG-
CCTTGGCCCCAG 3';
MOJH3FOR 5' TGCAGAGACGGTGACCAGAGTC-
CCTTGGCCCCAG 3';
MOJH4FOR 5' TGAGGAGACGGTGACCGAGGT-
TCCTTGACCCAG 3';
HUJH1FOR 5' TGAGGAGACGGTGACCAGGGTG-
CCCTGGCCCCAG 3';
HUJH2FOR 5' TGAGGAGACGGTGACCAGGGTG-
CCACGGCCCCAG 3';
HUJH4FOR 5' TGAGGAGACGGTGACCAGGGT-

TCCTTGGCCCCAG 3';
VK1FOR 5' GTTAGATCTCCAGCTTGGTCCC 3';
VK2FOR 5' CGTTAGATCTCCAGCTTGGTCCC 3';
VK3FOR 5' CCGTTTCAGCTCGAGCTTGGTCCC
3';
5 MOJK1FOR 5' CGTTAGATCTCCAGCTTGGTGCC
3';
MOJK3FOR 5' GGTTAGATCTCCAGCTTGGTCCC
3';
10 MOJK4FOR 5' CGTTAGATCTCCAACCTTGTCCC
3';
HUJK1FOR 5' CGTTAGATCTCCACCTTGGTCCC
3';
HUJK3FOR 5' CGTTAGATCTCCACCTTGGTCCC
3';
15 HUJK4FOR 5' CGTTAGATCTCCACCTTGGTCCC
3';
HUJK5FOR 5' CGTTAGATCTCCAGTCGTGTCCC
3';
20 VH1BACK 5' AGGT(C/G)(C/A)A(G/A)CTGCAG-
(G/C)AGTC(T/A)GG 3';
Hu2VHIBACK: 5' CAGGTGCAGCTGCAG-
CAGTCTGG 3';
HuVHIBACK: 5' CAGGTGCAGCTGCAG-
GAGTCGGG 3';
25 Hu2VHIIIBACK: 5' GAGGTGCAGCTGCAG-
GAGTCTGG 3';
HuVHIVBACK: 5' CAGGTGCAGCTGCAG-
CAGTCTGG 3';
30 MOVHIBACK 5' AGGTGCAGCTGCAGGAGTCAG
3';
MOVHIIABACK 5' AGGTCCAGCTGCAGCA(G/A)-
TCTGG 3';
MOVHIIIBACK 5' AGGTCCAAGCTGCAG-
35 CAGCCTGG 3';
; MOVHIBACK 5' AGGTGAAGCTGCAG-
GAGTCTGG 3';
VK1BACK 5' GACATTGAGCTGACCCAGTCTCCA
3';
40 VK2BACK 5' GACATTGAGCTCACCCAGTCTCCA
3';
MOVKIIABACK 5' GATGTTGAGCTGACCCAAAC-
TCCA 3';
MOVKIIIBACK 5' GATATTCAGCTGACCCAGGAT-
45 GAA 3';
HuHep1FOR 5' C(A/G)(C/G)-
TGAGCTCACTGTGTCTCTCGACA 3';
HuOcta1BACK 5' CGTGAATATGCAAATAA 3';
HuOcta2BACK 5' AGTAGGAGACATGCAAAT 3';
50 and
HuOcta3BACK 5' CACCACCCACATGCAAAT 3';
VHMUT1 5' GGAGACGGTGACCGTGGTCCCTTG-
GCCCCAGTAGTCAAG
NNNNNNNNNNNNCTCTCTGGC 3' (where N is an
55 equimolar mixture of T, C, G and A)
M13 pPRIMER 5' AACAGCTATGACCATG 3' (New
England Biolabs "1201)

EXAMPLE 1Cloning of Mouse Rearranged Variable region genes from hybridomas, assembly of genes encoding chimaeric antibodies and the expression of antibodies from myeloma cells

VH1FOR is designed to anneal with the 3' end of the sense strand of any mouse heavy chain variable domain encoding sequence. It contains a BstEII recognition site. VK1FOR is designed to anneal with the 3' end of the sense strand of any mouse kappa-type light chain variable domain encoding sequence and contains a BglII recognition site. VH1BACK is designed to anneal with the 3' end of the antisense strand of any mouse heavy chain variable domain and contains a PstI recognition site. VK1BACK is designed to anneal with the 3' end of the antisense strand of any mouse kappa-type light chain variable domain encoding sequence and contains a PvuII recognition site.

In this Example five mouse hybridomas were used as a source of ds nucleic acid. The hybridomas produce monoclonal antibodies (MAbs) designated MBr1 [23], BW431/26 [24], BW494/32 [25], BW250/183 [24,26] and BW704/152 [27]. MAB MBr1 is particularly interesting in that it is known to be specific for a saccharide epitope on a human mammary carcinoma line MCF-7 [28].

Cloning via mRNA

Each of the five hybridomas referred to above was grown up in roller bottles and about 5×10^8 cells of each hybridoma were used to isolate RNA. mRNA was separated from the isolated RNA using oligodT cellulose [29]. First strand cDNA was synthesised according to the procedure described by Maniatis et al. [30] as set out below.

In order to clone the heavy chain variable domain encoding sequence, a 50 μ l reaction solution which contains 10 μ g mRNA, 20 pmole VH1FOR primer, 250 μ M each of dATP, dTTP, dCTP and dGTP, 10 mM dithiothreitol (DTT), 100 mM Tris.HCl, 10 mM MgCl₂ and 140 mM KCl, adjusted to pH 8.3 was prepared. The reaction solution was heated at 70°C for ten minutes and allowed to cool to anneal the primer to the 3' end of the variable domain encoding sequence in the mRNA. To the reaction solution was then added 46 units of reverse transcriptase (Anglian Biotec) and the solution was then incubated at 42°C for 1 hour to cause first strand cDNA synthesis.

In order to clone the light chain variable domain encoding sequence, the same procedure as set out above was used except that the VK1FOR

primer was used in place of the VH1FOR primer.

Amplification from RNA/DNA hybrid

Once the ds RNA/DNA hybrids had been produced, the variable domain encoding sequences were amplified as follows. For heavy chain variable domain encoding sequence amplification, a 50 μ l reaction solution containing 5 μ l of the ds RNA/DNA hybrid-containing solution, 25 pmole each of VH1FOR and VH1BACK primers, 250 μ M of dATP, dTTP, dCTP and dGTP, 67 mM Tris.HCl, 17 mM ammonium sulphate, 10 mM MgCl₂, 200 μ g/ml gelatine and 2 units Taq polymerase (Cetus) was prepared. The reaction solution was overlaid with paraffin oil and subjected to 25 rounds of temperature cycling using a Techne PHC-1 programmable heating block. Each cycle consisted of 1 minute and 95°C (to denature the nucleic acids), 1 minute at 30°C (to anneal the primers to the nucleic acids) and 2 minutes at 72°C (to cause elongation from the primers). After the 25 cycles, the reaction solution and the oil were extracted twice with ether, once with phenol and once with phenol/CHCl₃. Thereafter ds cDNA was precipitated with ethanol. The precipitated ds cDNA was then taken up in 50 μ l of water and frozen.

The procedure for light chain amplification was exactly as described above, except that the VK1FOR and VK1BACK primers were used in place of the VH1FOR and VH1BACK primers respectively.

5 μ l of each sample of amplified cDNA was fractionated on 2% agarose gels by electrophoresis and stained with ethidium bromide. This showed that the amplified ds cDNA gave a major band of the expected size (about 330 bp). (However the band for VK DNA of MBr1 was very weak. It was therefore excised from the gel and reamplified in a second round.) Thus by this simple procedure, reasonable quantities of ds DNA encoding the light and heavy chain variable domains of the five MAbs were produced.

Heavy Chain Vector Construction

A BstEII recognition site was introduced into the vector M13-HuVHNP [31] by site directed mutagenesis [32,33] to produce the vector M13-VHPCR1 (Figures 2 and 3).

Each amplified heavy chain variable domain encoding sequence was digested with the restriction enzymes PstI and BstEII. The fragments were phenol extracted, purified on 2% low melting point agarose gels and force cloned into vector M13-VHPCR1 which had been digested with PstI and

BstEII and purified on an 0.8% agarose gel. Clones containing the variable domain inserts were identified directly by sequencing [34] using primers based in the 3' non-coding variable region in the M13-VHPCR1 vector.

There is an internal PstI site in the heavy chain variable domain encoding sequences of BW431/26. This variable domain encoding sequence was therefore assembled in two steps. The 3' PstI-BstEII fragment was first cloned into M13-VHPCR1, followed in a second step by the 5' PstI fragment.

Light Chain Vector Construction

Vector M13mp18 [35] was cut with PvuII and the vector backbone was blunt ligated to a synthetic HindIII-BamHI polylinker. Vector M13-HuV-KLYS [36] was digested with HindIII and BamHI to isolate the HuVKLYS gene. This HindIII-BamHI fragment was then inserted into the HindIII-BamHI polylinker site to form a vector M13-VKPCR1 which lacks any PvuII sites in the vector backbone (Figures 4 and 5). This vector was prepared in *E. coli* JM110 [22] to avoid dam methylation at the BclI site.

Each amplified light chain variable domain encoding sequence was digested with PvuII and BglII. The fragments were phenol extracted, purified on 2% low melting point agarose gels and force cloned into vector M13-VKPCR1 which had been digested with PvuII and BclI, purified on an 0.8% agarose gel and treated with calf intestinal phosphatase. Clones containing the light chain variable region inserts were identified directly by sequencing [34] using primers based in the 3' non-coding region of the variable domain in the M13-VKPCR1 vector.

The nucleotide sequences of the MBr1 heavy and light chain variable domains are shown in Figure 6 with part of the flanking regions of the M13-VHPCR1 and M13-VKPCR1 vectors.

Antibody Expression

The HindIII-BamHI fragment carrying the MBr1 heavy chain variable domain encoding sequence in M13-VHPCR1 was recloned into a pSV-gpt vector with human γ 1 constant regions [37] (Figure 7). The MBr1 light chain variable domain encoding sequence in M13-VKPCR1 was recloned as a HindIII-BamHI fragment into a pSV vector, pSV-hyg-HuCK with a hygromycin resistance marker and a human kappa constant domain (Figure 8). The assembly of the genes is summarised in Figure 9.

The vectors thus produced were linearised with

PvuII (in the case of the pSV-hygro vectors the PvuII digest is only partial) and cotransfected into the non-secreting mouse myeloma line NSO [38] by electroporation [39]. One day after cotransfection, cells were selected in 0.3 μ g/ml mycophenolic acid (MPA) and after seven days in 1 μ g/ml MPA. After 14 days, four wells, each containing one or two major colonies, were screened by incorporation of 14 C-lysine [40] and the secreted antibody detected after precipitation with protein-A Sepharose™ (Pharmacia) on SDS-PAGE [41]. The gels were stained, fixed, soaked in a fluorographic reagent, Amplify™ (Amersham), dried and autoradiographed on preflashed film at -70°C for 2 days.

Supernatant was also tested for binding to the mammary carcinoma line MCF-7 and the colon carcinoma line HT-29, essentially as described by Menard et al. [23], either by an indirect immunofluorescence assay on cell suspensions (using a fluorescein-labelled goat anti-human IgG (Amersham)) or by a solid phase RIA on monolayers of fixed cells (using 125 I-protein A (Amersham)).

It was found that one of the supernatants from the four wells contained secreted antibody. The chimeric antibody in the supernatant, like the parent mouse MBr1 antibody, was found to bind to MCF-7 cells but not the HT-29 cells, thus showing that the specificity had been properly cloned and expressed.

Example 2

Cloning of rearranged variable genes from genomic DNA of mouse spleen

Preparation of DNA from spleen.

The DNA from the mouse spleen was prepared in one of two ways (although other ways can be used).

Method 1.

A mouse spleen was cut into two pieces and each piece was put into a standard Eppendorf tube with 200 μ l of PBS. The tip of a 1 ml glass pipette was closed and rounded in the blue flame of a Bunsen burner. The pipette was used to squash the spleen piece in each tube. The cells thus produced were transferred to a fresh Eppendorf tube and the method was repeated three times until the connective tissue of the spleen appeared white. Any connective tissue which has been trans-

ferred with the cells was removed using a drawn-out Pasteur pipette. The cells were then washed in PBS and distributed into four tubes.

The mouse spleen cells were then sedimented by a 2 minute spin in a Microcentaur centrifuge at low speed setting. All the supernatant was aspirated with a drawn out Pasteur pipette. If desired, at this point the cell sample can be frozen and stored at -20°C .

To the cell sample (once thawed if it had been frozen) was added 500 μl of water and 5 μl of a 10% solution of NP-40, a non-ionic detergent. The tube was closed and a hole was punched in the lid. The tube was placed on a boiling water bath for 5 minutes to disrupt the cells and was then cooled on ice for 5 minutes. The tube was then spun for 2 minutes at high speed to remove cell debris.

The supernatant was transferred to a new tube and to this was added 125 μl 5M NaCl and 30 μl 1M MOPS adjusted to pH 7.0. The DNA in the supernatant was absorbed on a Qiagen 5 tip and purified following the manufacturer's instructions for lambda DNA. After isopropanol precipitation, the DNA was resuspended in 500 μl water.

Method 2.

This method is based on the technique described in Maniatis et al. [30]. A mouse spleen was cut into very fine pieces and put into a 2 ml glass homogeniser. The cells were then freed from the tissue by several slow up and down strokes with the piston. The cell suspension was made in 500 μl phosphate buffered saline (PBS) and transferred to an Eppendorf tube. The cells were then spun for 2 min at low speed in a Microcentaur centrifuge. This results in a visible separation of white and red cells. The white cells, sedimenting slower, form a layer on top of the red cells. The supernatant was carefully removed and spun to ensure that all the white cells had sedimented. The layer of white cells was resuspended in two portions of 500 μl PBS and transferred to another tube.

The white cells were precipitated by spinning in the Microcentaur centrifuge at low speed for one minute. The cells were washed a further two times with 500 μl PBS, and were finally resuspended in 200 μl PBS. The white cells were added to 2.5 ml 25 mM EDTA and 10 mM Tris.Cl, pH 7.4, and vortexed slowly. While vortexing 25 μl 20% SDS was added. The cells lysed immediately and the solution became viscous and clear. 100 μl of 20 mg/ml proteinase K was added and incubated one to three hours at 50°C .

The sample was extracted with an equal volume of phenol and the same volume of chloroform, and vortexed. After centrifuging, the aqueous phase

was removed and 1/10 volume 3M ammonium acetate was added. This was overlaid with three volumes of cold ethanol and the tube rocked carefully until the DNA strands became visible. The DNA was spooled out with a Pasteur pipette, the ethanol allowed to drip off, and the DNA transferred to 1 ml of 10 mM Tris.Cl pH 7.4, 0.1 mM EDTA in an Eppendorf tube. The DNA was allowed to dissolve in the cold overnight on a roller.

Amplification from genomic DNA.

The DNA solution was diluted 1/10 in water and boiled for 5 min prior to using the polymerase chain reaction (PCR). For each PCR reaction, typically 50-200 ng of DNA were used.

The heavy and light chain variable domain encoding sequences in the genomic DNA isolated from the human PBL or the mouse spleen cells was then amplified and cloned using the general protocol described in the first two paragraphs of the section headed "Amplification from RNA/DNA Hybrid" in Example 1, except that during the annealing part of each cycle, the temperature was held at 65°C and that 30 cycles were used. Furthermore, to minimise the annealing between the 3' ends of the two primers, the sample was first heated to 95°C , then annealed at 65°C , and only then was the Taq polymerase added. At the end of the 30 cycles, the reaction mixture was held at 60°C for five minutes to ensure that complete elongation and renaturation of the amplified fragments had taken place.

The primers used to amplify the mouse spleen genomic DNA were VH1FOR and VH1BACK, for the heavy chain variable domain and VK2FOR and VK1BACK, for the light chain variable domain. (VK2FOR only differs from VK1FOR in that it has an extra C residue on the 5' end.)

Other sets of primers, designed to optimise annealing with different families of mouse VH and V κ genes were devised and used in mixtures with the primers above. For example, mixtures of VK1FOR, MOJK1FOR, MOJK3FOR and MOJK4FOR were used as forward primers and mixtures of VK1BACK, MOVK1IBACK and MOVK1IIBACK as back primers for amplification of V κ genes. Likewise mixtures of VH1FOR, MOJH1FOR, MOJH2FOR, MOJH3FOR and MOJH4FOR were used as forward primers and mixtures of VH1BACK, MOVH1IBACK, MOVH1IIBACK, MOVH2IBACK, MOVH2IIBACK were used as backward primers for amplification of VH genes.

All the heavy chain FOR primers referred to above contain a BstEII site and all the BACK primers referred to above contain a PstI site. The light chain FOR and BACK primers referred to

above all contain BglII and PvuII sites respectively. Light chain primers (VK3FOR and VK2BACK) were also devised which utilised different restriction sites, SacI and XhoI.

Typically all these primers yielded amplified DNA of the correct size on gel electrophoresis, although other bands were also present. However, a problem was identified in which the 5' and 3' ends of the forward and backward primers for the VH genes were partially complementary, and this could yield a major band of "primer-dimer" in which the two oligonucleotides prime on each other. For this reason an improved forward primer, VH1FOR-2 was devised in which the two 3' nucleotides were removed from VH1FOR.

Thus, the preferred amplification conditions for mouse VH genes are as follows: the sample was made in a volume of 50-100 µl, 50-100 ng of DNA, VH1FOR-2 and VH1BACK primers (25 pmole of each), 250 µM of each deoxynucleotide triphosphate, 10 mM Tris.HCl, pH 8.8, 50 mM KCl, 1.5 mM MgCl₂, and 100 µg/ml gelatine. The sample was overlaid with paraffin oil, heated to 95° C for 2 min, 65° C for 2 min, and then to 72° C: taq polymerase was added after the sample had reached the elongation temperature and the reaction continued for 2 min at 72° C. The sample was subjected to a further 29 rounds of temperature cycling using the Techne PHC-1 programmable heating block.

The preferred amplification conditions for mouse Vκ genes from genomic DNA are as follows: the sample treated as above except with Vκ primers, for example VK3FOR and VK2BACK, and using a cycle of 94° C for one minute, 60° C for one minute and 72° C for one minute.

The conditions which were devised for genomic DNA are also suitable for amplification from the cDNA derived from mRNA from mouse spleen or mouse hybridoma.

Cloning and analysis of variable region genes

The reaction mixture was then extracted twice with 40 µl of water-saturated diethyl ether. This was followed by a standard phenol extraction and ethanol precipitation as described in Example 1. The DNA pellet was then dissolved in 100 µl 10 mM Tris.Cl, 0.1 mM EDTA.

Each reaction mixture containing a light chain variable domain encoding sequence was digested with SacI and XhoI (or with PvuII and BglII) to enable it to be ligated into a suitable expression vector. Each reaction mixture containing a heavy chain variable domain encoding sequence was digested with PstI and BstEII for the same purpose.

The heavy chain variable genes isolated as

above from a mouse hyperimmunised with lysozyme were cloned into M13VHPCR1 vector and sequenced. The complete sequences of 48 VH gene clones were determined (Figure 10). All but two of the mouse VH gene families were represented, with frequencies of: VA (1), IIIC (1), IIIB (8), IIIA (3), IIB (17), IIA (2), IB (12), IA (4). In 30 clones, the D segments could be assigned to families SP2 (14), FL16 (11) and Q52 (5), and in 38 clones the JH minigenes to families JH1 (3), JH2 (7), JH3 (14) and JH4 (14). The different sequences of CDR3 marked out each of the 48 clones as unique. Nine pseudogenes and 16 unproductive rearrangements were identified. Of the clones sequenced, 27 have open reading frames.

Thus the method is capable of generating a diverse repertoire of heavy chain variable genes from mouse spleen DNA.

Example 3

Cloning of rearranged variable genes from mRNA from human peripheral blood lymphocytes

Preparation of mRNA.

Human peripheral blood lymphocytes were purified and mRNA prepared directly (Method 1), or mRNA was prepared after addition of Epstein Barr virus (Method 2).

Method 1.

20 ml of heparinised human blood from a healthy volunteer was diluted with an equal volume of phosphate buffered saline (PBS) and distributed equally into 50 ml Falcon tubes. The blood was then underlaid with 15ml Ficoll Hypaque (Pharmacia 10-A-001-07). To separate the lymphocytes from the red blood cells, the tubes were spun for 10 minutes at 1800 rpm at room temperature in an IEC Centra 3E table centrifuge. The peripheral blood lymphocytes (PBL) were then collected from the interphase by aspiration with a Pasteur pipette. The cells were diluted with an equal volume of PBS and spun again at 1500 rpm for 15 minutes. The supernatant was aspirated, the cell pellet was resuspended in 1 ml PBS and the cells were distributed into two Eppendorf tubes.

Method 2.

40 ml human blood from a patient with HIV in

the pre-AIDS condition was layered on Ficoll to separate the white cells (see Method 1 above). The white cells were then incubated in tissue culture medium for 4-5 days. On day 3, they were infected with Epstein Barr virus. The cells were pelleted (approx 2×10^7 cells) and washed in PBS.

The cells were pelleted again and lysed with 7 ml 5M guanidine isothiocyanate, 50 mM Tris, 10 mM EDTA, 0.1 mM dithiothreitol. The cells were vortexed vigorously and 7 volumes of 4M LiCl added. The mixture was incubated at 4°C for 15-20 hrs. The suspension was spun and the supernatant resuspended in 3M LiCl and centrifuged again. The pellet was dissolved in 2ml 0.1 % SDS, 10 mM Tris HCl and 1 mM EDTA. The suspension was frozen at -20°C , and thawed by vortexing for 20 s every 10 min for 45 min. A large white pellet was left behind and the clear supernatant was extracted with phenol chloroform, then with chloroform. The RNA was precipitated by adding 1/10 volume 3M sodium acetate and 2 vol ethanol and leaving overnight at -20°C . The pellet was suspended in 0.2 ml water and reprecipitated with ethanol. Aliquots for cDNA synthesis were taken from the ethanol precipitate which had been vortexed to create a fine suspension.

100 μl of the suspension was precipitated and dissolved in 20 μl water for cDNA synthesis [30] using 10 pmole of a HUFOR primer (see below) in final volume of 50 μl . A sample of 5 μl of the cDNA was amplified as in Example 2 except using the primers for the human VH gene families (see below) using a cycle of 95°C , 60°C and 72°C .

The back primers for the amplification of human DNA were designed to match the available human heavy and light chain sequences, in which the different families have slightly different nucleotide sequences at the 5' end. Thus for the human VH genes, the primers Hu2VHIBACK, HuVHIIIBACK, Hu2VHIIIBACK and HuVH1VBACK were designed as back primers, and HUJH1FOR, HUJH2FOR and HUJH4FOR as forward primers based entirely in the variable gene. Another set of forward primers Hu1VHFOR, Hu2VHFOR, Hu3VHFOR, and Hu4VHFOR was also used, which were designed to match the human J-regions and the 5' end of the constant regions of different human isotopes.

Using sets of these primers it was possible to demonstrate a band of amplified ds cDNA by gel electrophoresis.

One such experiment was analysed in detail to establish whether there was a diverse repertoire in a patient with HIV infection. It is known that during the course of AIDS, that T-cells and also antibodies are greatly diminished in the blood. Presumably the repertoire of lymphocytes is also diminished. In this experiment, for the forward priming, an

equimolar mixture of primers Hu1VHFOR, Hu2VHFOR, Hu3VHFOR, and Hu4VHFOR (in PCR 25 pmole of primer 5' ends) was used. For the back priming, the primers Hu2VHIBACK, HuVHIIIBACK, Hu2VHIIIBACK and HuVH1VBACK were used separately in four separate primings. The amplified DNA from the separate primings was then pooled, digested with restriction enzymes PstI and BstEII as above, and then cloned into the vector M13VHPCR1 for sequencing. The sequences reveal a diverse repertoire (Fig. 11) at this stage of the disease.

For human V α genes the primers HuJK1FOR, HUJK3FOR, HUJK4FOR and HUJK5FOR were used as forward primers and VK1BACK as back primer. Using these primers it was possible to see a band of amplified ds cDNA of the correct size by gel electrophoresis.

Example 4

Cloning of unrearranged variable gene genomic DNA from human peripheral blood lymphocytes

Human peripheral blood lymphocytes of a patient with non-Hodgkins lymphoma were prepared as in Example 3 (Method 1). The genomic DNA was prepared from the PBL using the technique described in Example 2 (Method 2). The VH region in the isolated genomic DNA was then amplified and cloned using the general protocol described in the first two paragraphs of the section headed "Amplification from RNA/DNA hybrid" in Example 1 above, except that during the annealing part of each cycle, the temperature was held at 55°C and that 30 cycles were used. At the end of the 30 cycles, the reaction mixture was held at 60°C for five minutes to ensure that complete elongation and renaturation of the amplified fragments had taken place.

The forward primer used was HuHep1FOR, which contains a SacI site. This primer is designed to anneal to the 3' end of the unrearranged human VH region gene, and in particular includes a sequence complementary to the last three codons in the VH region gene and nine nucleotides downstream of these three codons.

As the back primer, an equimolar mixture of HuOcta1BACK, HuOcta2BACK and HuOcta3BACK was used. These primers anneal to a sequence in the promoter region of the genomic DNA VH gene (see Figure 1). 5 μl of the amplified DNA was checked on 2% agarose gels in TBE buffer and stained with thidium bromide. A double band was seen of about 620 nucleotides which corresponds to the size expected for the unrearranged VH gene.

The ds cDNA was digested with SacI and cloned into an M13 vector for sequencing. Although there are some sequences which are identical, a range of different unrearranged human VH genes were identified (Figure 12).

Example 5

Cloning Variable Domains with Binding Activities from a Hybridoma

The heavy chain variable domain (VHLYS) of the D1.3 (anti-lysozyme) antibody was cloned into a vector similar to that described previously [42] but under the control of the lac z promoter, such that the VHLYS domain is attached to a pelB leader sequence for export into the periplasm. The vector was constructed by synthesis of the pelB leader sequence [43], using overlapping oligonucleotides, and cloning into a pUC 19 vector [35]. The VHLYS domain of the D1.3 antibody was derived from a cDNA clone [44] and the construct (pSW1) sequenced (Figure 13).

To express both heavy and light chain variable domains together, the light chain variable region (VKLYS) of the D1.3 antibody was introduced into the pSW1 vector, with a pelB signal sequence to give the construct pSW2 (Figure 14).

A strain of *E. coli* (BMH71-18) [45] was then transformed [46,47] with the plasmid pSW1 or pSW2, and colonies resistant to ampicillin (100 µg/ml) were selected on a rich (2 x TY = per litre of water, 16g Bacto-tryptone, 10g yeast extract, 5g NaCl) plate which contained 1% glucose to repress the expression of variable domain(s) by catabolite repression.

The colonies were inoculated into 50 ml 2 x TY (with 1% glucose and 100 µg/ml ampicillin) and grown in flasks at 37°C with shaking for 12-16 hr. The cells were centrifuged, the pellet washed twice with 50 mM sodium chloride, resuspended in 2 x TY medium containing 100 µg/ml ampicillin and the inducer IPTG (1 mM) and grown for a further 30 hrs at 37°C. The cells were centrifuged and the supernatant was passed through a Nalgene filter (0.45 µm) and then down a 1 - 5 ml lysozyme-Sepharose affinity column. (The column was derived by coupling lysozyme at 10 mg/ml to CNBr activated Sepharose.) The column was first washed with phosphate buffered saline (PBS), then with 50 mM diethylamine to elute the VHLYS domain (from pSW1) or VHLYS in association with VKLYS (from pSW2).

The VHLYS and VKLYS domains were identified by SDS polyacrylamide electrophoresis as the correct size. In addition, N-terminal sequence

d termination of VHLYS and VKLYS isolated from a polyacrylamide gel showed that the signal peptid had been produced correctly. Thus both the Fv fragment and the VHLYS domains are able to bind to the lysozyme affinity column, suggesting that both retain at least some of the affinity of the original antibody.

The size of the VHLYS domain was compared by FPLC with that of the Fv fragment on Superose 12. This indicates that the VHLYS domain is a monomer. The binding of the VHLYS and Fv fragment to lysozyme was checked by ELISA, and equilibrium and rapid reaction studies were carried out using fluorescence quench.

The ELISA for lysozyme binding was undertaken as follows:

(1) The plates (Dynatech Immulon) were coated with 200 µl per well of 300 µg/ml lysozyme in 50 mM NaHCO₃, pH 9.6 overnight at room temperature;

(2) The wells were rinsed with three washes of PBS, and blocked with 300 µl per well of 1% Sainsbury's instant dried skimmed milk powder in PBS for 2 hours at 37°C;

(3) The wells were rinsed with three washes of PBS and 200 µl of VHLYS or Fv fragment (VHLYS associated with VKLYS) were added and incubated for 2 hours at room temperature;

(4) The wells were washed three times with 0.05% Tween 20 in PBS and then three times with PBS to remove detergent;

(5) 200 µl of a suitable dilution (1:1000) of rabbit polyclonal antisera raised against the Fv fragment in 2% skimmed milk powder in PBS was added to each well and incubated at room temperature for 2 hours;

(6) Washes were repeated as in (4);

(7) 200 µl of a suitable dilution (1:1000) of goat anti-rabbit antibody (ICN Immunochemicals) coupled to horse radish peroxidase, in 2% skimmed milk powder in PBS, was added to each well and incubated at room temperature for 1 hour;

(8) Washes were repeated as in (4); and

(9) 200 µl 2,2'-azino-bis(3-ethylbenz-thiazolinesulphonic acid) [Sigma] (0.55 mg/ml, with 1 µl 20% hydrogen peroxide: water per 10 ml) was added to each well and the colour allowed to develop for up to 10 minutes at room temperature.

The reaction was stopped by adding 0.05% sodium azide in 50 mM citric acid pH 4.3. ELISA plates were read in a Titertek Multiscan plate reader. Supernatant from the induced bacterial cultures of both pSW1 (VHLYS domain) or pSW2 (Fv fragment) was found to bind to lysozyme in the ELISA.

The purified VHLYS and Fv fragments were titrated with lysozyme using fluorescence quench (Perkin Elmer LS5B Luminescence Spectrometer) to measure the stoichiometry of binding and the

affinity constant for lysozyme [48,49]. The titration of the Fv fragment at a concentration of 30 nM indicates a dissociation constant of 2.8 nM using a Scatchard analysis.

A similar analysis using fluorescence quench and a Scatchard plot was carried out for VHLYS, at a VHLYS concentration of 100 nM. The stoichiometry of antigen binding is about 1 mole of lysozyme per mole of VHLYS (calculated from plot). (The concentration of VH domains was calculated from optical density at 280 nM using the typical extinction coefficient for complete immunoglobulins.) Due to possible errors in measuring low optical densities and the assumption about the extinction coefficient, the stoichiometry was also measured more carefully. VHLYS was titrated with lysozyme as above using fluorescence quench. To determine the concentration of VHLYS a sample of the stock solution was removed, a known amount of nor-leucine added, and the sample subjected to quantitative amino acid analysis. This showed a stoichiometry of 1.2 mole of lysozyme per mole of VHLYS domain. The dissociation constant was calculated at about 12 nM.

The on-rates for VHLYS and Fv fragments with lysozyme were determined by stopped-flow analysis (Hi Tech Stop Flow SHU machine) under pseudo-first order conditions with the fragment at a ten fold higher concentration than lysozyme [50]. The concentration of lysozyme binding sites was first measured by titration with lysozyme using fluorescence quench as above. The on rates were calculated per mole of binding site (rather than amount of VHLYS protein). The on-rate for the Fv fragment was found to be $2.2 \times 10^6 \text{ M}^{-1} \text{ s}^{-1}$ at 25°C . The on-rate for the VHLYS fragment found to be $3.8 \times 10^6 \text{ M}^{-1} \text{ s}^{-1}$ and the off-rate 0.075 s^{-1} at 20°C . The calculated affinity constant is 19 nM. Thus the VHLYS binds to lysozyme with a dissociation constant of about 19 nM, compared with that of the Fv of 3 nM.

Example 6

Cloning complete variable domains with binding activities from mRNA or DNA of antibody-secreting cells

A mouse was immunised with hen egg white lysozyme (100 μg i.p. day 1 in complete Freund's adjuvant), after 14 days immunised i.p. again with 100 μg lysozyme with incomplete Freund's adjuvant, and on day 35 i.v. with 50 μg lysozyme in saline. On day 39, spleen was harvested. A second mouse was immunised with keyhole limpet haemocyanin (KLH) in a similar way. The DNA was

prepared from the spleen according to Example 2 (Method 2). The VH genes were amplified according to the preferred method in Example 2.

Human peripheral blood lymphocytes from a patient infected with HIV were prepared as in Example 3 (Method 2) and mRNA prepared. The VH genes were amplified according to the method described in Example 3, using primers designed for human VH gene families.

After the PCR, the reaction mixture and oil were extracted twice with ether, once with phenol and once with phenol/ CHCl_3 . The double stranded DNA was then taken up in 50 μl of water and frozen. 5 μl was digested with PstI and BstEII (encoded within the amplification primers) and loaded on an agarose gel for electrophoresis. The band of amplified DNA at about 350 bp was extracted.

Expression of anti-lysozyme activities

The repertoire of amplified heavy chain variable domains (from mouse immunised with lysozyme and from human PBLs) was then cloned directly into the expression vector pSW1HPOLYMYC. This vector is derived from pSW1 except that the VHLYS gene has been removed and replaced by a polylinker restriction site. A sequence encoding a peptide tag was inserted (Figure 15). Colonies were toothpicked into 1 ml cultures. After induction (see Example 5 for details), 10 μl of the supernatant from fourteen 1 ml cultures was loaded on SDS-PAGE gels and the proteins transferred electrophoretically to nitrocellulose. The blot was probed with antibody 9E10 directed against the peptide tag.

The probing was undertaken as follows. The nitrocellulose filter was incubated in 3% bovine serum albumin (BSA)/TBS buffer for 20 min (10 x TBS buffer is 100 mM Tris.HCl, pH 7.4, 9% w/v NaCl). The filter was incubated in a suitable dilution of antibody 9E10 (about 1/500) in 3% BSA/TBS for 1 - 4 hrs. After three washes in TBS (100 ml per wash, each wash for 10 min), the filter was incubated with 1:500 dilution of anti-mouse antibody (peroxidase conjugated anti-mouse Ig (Dakopats)) in 3% BSA/TBS for 1 - 2 hrs. After three washes in TBS and 0.1% Triton X-100 (about 100 ml per wash, each wash for 10 min), a solution containing 10 ml chloronaphthol in methanol (3 mg/ml), 40 ml TBS and 50 μl hydrogen peroxide solution was added over the blot and allowed to react for up to 10 min. The substrate was washed out with excess water. The blot revealed bands similar in mobility to VHLYSMYC on the Western blot, showing that other VH domains could be expressed.

Colonies were then toothpicked individually into

wells of an ELISA plate (200 μ l) for growth and induction. They were assayed for lysozyme binding with the 9E10 antibody (as in Examples 5 and 7). Wells with lysozyme-binding activity were identified. Two positive wells (of 200) were identified from the amplified mouse spleen DNA and one well from the human cDNA. The heavy chain variable domains were purified on a column of lysozyme-Sepharose. The affinity for lysozyme of the clones was estimated by fluorescence quench titration as >50 nM. The affinities of the two clones (VH3 and VH8) derived from the mouse genes were also estimated by stop flow analysis (ratio of k_{on}/k_{off}) as 12 nM and 27 nM respectively. Thus both these clones have a comparable affinity to the VHLYS domain. The encoded amino acid sequences of VH3 and VH8 are given in Figure 16, and that of the human variable domain in Figure 17.

A library of VH domains made from the mouse immunised with lysozyme was screened for both lysozyme and keyhole limpet haemocyanin (KLH) binding activities. Two thousand colonies were toothpicked in groups of five into wells of ELISA plates, and the supernatants tested for binding to lysozyme coated plates and separately to KLH coated plates. Twenty one supernatants were shown to have lysozyme binding activities and two to have KLH binding activities. A second expression library, prepared from a mouse immunised with KLH was screened as above. Fourteen supernatants had KLH binding activities and a single supernatant had lysozyme binding activity.

This shows that antigen binding activities can be prepared from single VH domains, and that immunisation facilitates the isolation of these domains.

Example 7

Cloning variable domains with binding activities by mutagenesis.

Taking a single rearranged VH gene, it may be possible to derive entirely new antigen binding activities by extensively mutating each of the CDRs. The mutagenesis might be entirely random, or be derived from pre-existing repertoires of CDRs. Thus a repertoire of CDR3s might be prepared as in the preceding examples by using "universal" primers based in the flanking sequences, and likewise repertoires of the other CDRs (singly or in combination). The CDR repertoires could be stitched into place in the flanking framework regions by a variety of recombinant DNA techniques.

CDR3 appears to be the most promising region

for mutagenesis as CDR3 is more variable in size and sequence than CDRs 1 and 2. This region would be expected to make a major contribution to antigen binding. The heavy chain variable region (VHLYS) of the anti-lysozyme antibody D1.3 is known to make several important contacts in the CDR3 region.

Multiple mutations were made in CDR3. The polymerase chain reaction (PCR) and a highly degenerate primer were used to make the mutations and by this means the original sequence of CDR3 was destroyed. (It would also have been possible to construct the mutations in CDR3 by cloning a mixed oligonucleotide duplex into restriction sites flanking the CDR or by other methods of site-directed mutagenesis). Mutants expressing heavy chain variable domains with affinities for lysozyme were screened and those with improved affinities or new specificities were identified.

The source of the heavy chain variable domain was an M13 vector containing the VHLYS gene. The body of the sequence encoding the variable region was amplified using the polymerase chain reaction (PCR) with the mutagenic primer VHMUT1 based in CDR3 and the M13 primer which is based in the M13 vector backbone. The mutagenic primer hypermutates the central four residues of CDR3 (Arg-Asp-Tyr-Arg). The PCR was carried out for 25 cycles on a Techne PHC-1 programmable heat block using 100 ng single stranded M13mp19SW0 template, with 25 pmol of VHMUT1 and the M13 primer, 0.5 mM each dNTP, 67mM Tris.HCl, pH 8.8, 10 mM MgCl₂, 17 mM (NH₄)₂SO₄, 200 μ g/ml gelatine and 2.5 units Taq polymerase in a final volume of 50 μ l. The temperature regime was 95°C for 1.5 min, 25°C for 1.5 min and 72°C for 3 min (However a range of PCR conditions could be used). The reaction products were extracted with phenol/chloroform, precipitated with ethanol and resuspended in 10 mM Tris. HCl and 0.1 mM EDTA, pH 8.0.

The products from the PCR were digested with PstI and BstEII and purified on a 1.5% LGT agarose gel in Tris acetate buffer using GeneClean (Bio 101, LaJolla). The gel purified band was ligated into pSW2HPOLY (Figure 19). (This vector is related to pSW2 except that the body of the VHLYS gene has been replaced by a polylinker.) The vector was first digested with BstEII and PstI and treated with calf-intestinal phosphatase. Aliquots of the reaction mix were used to transform E. coli BMH 71-18 to ampicillin resistance. Colonies were selected on ampicillin (100 μ g/ml) rich plates containing glucose at 0.8% w/v.

Colonies resulting from transfection were picked in pools of five into two 96 well Corning microtitre plates, containing 200 μ l 2 x TY medium and 100 μ l TY medium, 100 μ g/ml ampicillin and 1%

glucose. The colonies were grown for 24 hours at 37 °C and then cells were washed twice in 200 µl 50 mM NaCl, pelleting the cells in an IEC Centra-3 bench top centrifuge with microtitre plate head fitting. Plates were spun at 2,500 rpm for 10 min at room temperature. Cells were resuspended in 200 µl 2 x TY, 100 µg/ml ampicillin and 1 mM IPTG (Sigma) to induce expression, and grown for a further 24 hr.

Cells were spun down and the supernatants used in ELISA with lysozyme coated plates and anti-idiotypic sera (raised in rabbits against the Fv fragment of the D1.3 antibody). Bound anti-idiotypic serum was detected using horse radish peroxidase conjugated to anti-rabbit sera (ICN Immunochemicals). Seven of the wells gave a positive result in the ELISA. These pools were restreaked for single colonies which were picked, grown up, induced in microtitre plates and rescreened in the ELISA as above. Positive clones were grown up at the 50 ml scale and expression was induced. Culture supernatants were purified as in Example 5 on columns of lysozyme-Sepharose and eluates analysed on SDS-PAGE and staining with Page Blue 90 (BDH). On elution of the column with diethylamine, bands corresponding to the VHLYS mutant domains were identified, but none to the VKLYS domains. This suggested that although the mutant domains could bind to lysozyme, they could no longer associate with the VKLYS domains.

For seven clones giving a positive reaction in ELISA, plasmids were prepared and the VKLYS gene excised by cutting with EcoRI and religating. Thus the plasmids should only direct the expression of the VHLYS mutants. 1.5 ml cultures were grown and induced for expression as above. The cells were spun down and supernatant shown to bind lysozyme as above. (Alternatively the amplified mutant VKLYS genes could have been cloned directly into the pSW1HPOLY vector for expression of the mutant activities in the absence of VKLYS.)

An ELISA method was devised in which the activities of bacterial supernatants for binding of lysozyme (or KLH) were compared. Firstly a vector was devised for tagging of the VH domains at its C-terminal region with a peptide from the c-myc protein which is recognised by a monoclonal antibody 9E10. The vector was derived from pSW1 by a BstEII and SmaI double digest, and ligation of an oligonucleotide duplex made from

5' GTC ACC GTC TCC TCA GAA CAA AAA CTC
ATC TCA GAA GAG GAT CTG AAT TAA TAA 3'

and
5' TTA TTA ATT CAG ATC CTC TTC TGA GAT
GAG TTT TTG TTC TGA GGA GAC G 3'.

The VHLYSMYC protein domain expressed after induction was shown to bind to lysozyme and to

the 9E10 antibody by ELISA as follows:

(1) Falcon (3912) flat bottomed wells were coated with 180 µl lysozyme (3 mg/ml) or KLH (50 µg/ml) per well in 50 mM NaHCO₃, pH 9.6, and left to stand at room temperature overnight;

(2) The wells were washed with PBS and blocked for 2 hrs at 37 °C with 200 µl 2% Sainsbury's instant dried skimmed milk powder in PBS per well;

(3) The Blocking solution was discarded, and the wells washed out with PBS (3 washes) and 150 µl test solution (supernatant or purified tagged domain) pipetted into each well. The sample was incubated at 37 °C for 2 hrs;

(4) The test solution was discarded, and the wells washed out with PBS (3 washes). 100 µl of 4 µg/ml purified 9E10 antibody in 2% Sainsbury's instant dried skimmed milk powder in PBS was added, and incubated at 37 °C for 2 hrs;

(5) The 9E10 antibody was discarded, the wells washed with PBS (3 washes). 100 µl of 1/500 dilution of anti-mouse antibody (peroxidase conjugated anti-mouse Ig (Dakopats)) was added and incubated at 37 °C for 2 hrs;

(6) The second antibody was discarded and wells washed three times with PBS; and

(7) 100 µl 2,2' azino-bis(3-ethylbenz-thiazolinesulphonic acid) [Sigma] (0.55 mg/ml, with 1 µl 20% hydrogen peroxide: water per 10 ml) was added to each well and the colour allowed to develop for up to 10 minutes at room temperature.

The reaction was stopped by adding 0.05% sodium azide in 50 mM citric acid, pH 4.3. ELISA plates were read in an Titertek Multiscan plate reader.

The activities of the mutant supernatants were compared with VHLYS supernatant by competition with the VHLYSMYC domain for binding to lysozyme. The results show that supernatant from clone VHLYSMUT59 is more effective than wild type VHLYS supernatant in competing for VHLYSMYC. Furthermore, Western blots of SDS-PAGE aliquots of supernatant from the VHLYS and VHLYSMUT59 domain (using anti-Fv antisera) indicated comparable amounts of the two samples. Thus assuming identical amounts of VHLYS and VHLYSMUT59, the affinity of the mutant appears to be greater than that of the VHLYS domain.

To check the affinity of the VHLYSMUT59 domain directly, the clone was grown at the 1 l scale and 200-300 µg purified on lysozyme-Sepharose as in Example 5. By fluorescence quench titration of samples of VHLYS and VHLYSMUT59, the number of binding sites for lysozyme were determined. The samples of VHLYS and VHLYSMUT59 were then compared in the competition ELISA with VHLYSMYC over two orders of magnitude. In the competition assay each microtitre well contained a

constant amount of VHLYSMYC (approximately 0.6 μ g VHLYSMYC). Varying amounts of VHLYS or VHLYSMUT59 (3.8 μ M in lysozyme binding sites) were added (0.166 - 25 μ l). The final volume and buffer concentration in all wells was constant. 9E10 (anti-myc) antibody was used to quantitate bound VHLYSMYC in each assay well. The % inhibition of VHLYSMYC binding was calculated for each addition of VHLYS or VHLYSMUT59, after subtraction of background binding. Assays were carried out in duplicate. The results indicate that VHLYSMUT59 has a higher affinity for lysozyme than VHLYS.

The VHLYSMUT59 gene was sequenced (after recloning into M13) and shown to be identical to the VHLYS gene except for the central residues of CDR3 (Arg-Asp-Tyr-Arg). These were replaced by Thr-Gln-Arg-Pro: (encoded by ACACAAAGGCCA).

A library of 2000 mutant VH clones was screened for lysozyme and also for KLH binding (toothpicking 5 colonies per well as described in Example 6). Nineteen supernatants were identified with lysozyme binding activities and four with KLH binding activities. This indicates that new specificities and improved affinities can be derived by making a random repertoire of CDR3.

Example 8

Construction and expression of double domain for lysozyme binding.

The finding that single domains have excellent binding activities should allow the construction of strings of domains (concatamers). Thus, multiple specificities could be built into the same molecule, allowing binding to different epitopes spaced apart by the distance between domain heads. Flexible linker regions could be built to space out the domains. In principle such molecules could be devised to have exceptional specificity and affinity.

Two copies of the cloned heavy chain variable gene of the D1.3 antibody were linked by a nucleotide sequence encoding a flexible linker Gly-Gly-Gly-Ala-Pro-Ala-Ala-Ala-Pro-Ala-Gly-Gly-Gly- (by several steps of cutting, pasting and site directed mutagenesis) to yield the plasmid pSW3 (Figure 20). The expression was driven by a lacZ promoter and the protein was secreted into the periplasm via a pelB leader sequence (as described in Example 5 for expression of pSW1 and pSW2). The protein could be purified to homogeneity on a lysozyme affinity column. On SDS polyacrylamide gels, it gave a band of the right size (molecular weight about 26,000). The protein also bound strongly to lysozyme as detected by

ELISA (see Example 5) using anti-idiotypic antiserum directed against the Fv fragment of the D1.3 antibody to detect the protein. Thus, such constructs are readily made and secreted and at least one of the domains binds to lysozyme.

Example 9

Introduction of cysteine residue at C-terminal end of VHLYS

A cysteine residue was introduced at the C-terminus of the VHLYS domain in the vector pSW2. The cysteine was introduced by cleavage of the vector with the restriction enzymes BstI and SmaI (which excises the C-terminal portion of the J segment) and ligation of a short oligonucleotide duplex 5' GTC ACC GTC TCC TCA TGT TAA TAA 3' and 5' TTA TTA ACA TGA GGA GAC G 3'.

By purification on an affinity column of lysozyme Sepharose it was shown that the VHLYS-Cys domain was expressed in association with the VKLYS variable domain, but the overall yields were much lower than the wild type Fv fragment. Comparison of non-reducing and reducing SDS polyacrylamide gels of the purified Fv-Cys protein indicated that the two VH-Cys domains had become linked through the introduced cysteine residue.

Example 10

Linking of VH domain with enzyme

Linking of enzyme activities to VH domains should be possible by either cloning the enzyme on either the N-terminal or the C-terminal side of the VH domain. Since both partners must be active, it may be necessary to design a suitable linker (see Example 8) between the two domains. For secretion of the VH-enzyme fusion, it would be preferable to utilise an enzyme which is usually secreted. In Figure 21, there is shown the sequence of a fusion of a VH domain with alkaline phosphatase. The alkaline phosphatase gene was cloned from a plasmid carrying the *E. coli* alkaline phosphatase gene in a plasmid pEK48 [51] using the polymerase chain reaction. The gene was amplified with the primers

5' CAC CAC GGT CAC CGT CTC CTC ACG GAC ACC AGA AAT GCC TGT TCT G 3' and 5' GCG AAA ATT CAC TCC CGG GCG CGG TTT TAT TTC 3'. The gene was introduced into the vector pSW1 by cutting at BstEI and SmaI. The construction (Figure 21) was expressed in *E. coli*

strain BMH71-18 as in Example 5 and screened for phosphatase activity using 1 mg/ml p-nitrophenylphosphat as substrate in 10mM diethanolamine and 0.5 mM MgCl₂, pH 9.5) and also on SDS polyacrylamide gels which had been Western blotted (detecting with anti-idiotypic antiserum). No evidence was found for the secretion of the linked VHLYS-alkaline phosphatase as detected by Western blots (see Example 5), or for secretion of phosphatase activity.

However when the construct was transfected into a bacterial strain BL21DE3 [52] which is deficient in proteases, a band of the correct size (as well as degraded products) was detected on the Western blots. Furthermore phosphatase activity could now be detected in the bacterial supernatant. Such activity is not present in supernatant from the strain which had not been transfected with the construct.

A variety of linker sequences could then be introduced at the BstEI site to improve the spacing between the two domains.

Example 11

Coexpression of VH domains with Vk repertoire

A repertoire of V_x genes was derived by PCR using primers as described in Example 2 from DNA prepared from mouse spleen and also from mouse spleen mRNA using the primers VK3FOR and VK2BACK and a cycle of 94°C for 1 min, 60°C for 1 min, 72°C for 2 min. The PCR amplified DNA was fractionated on the agarose gel, the band excised and cloned into a vector which carries the VHLYS domain (from the D1.3 antibody), and a cloning site (SacI and XhoI) for cloning of the light chain variable domains with a myc tail (pSW1VHLYS-VKPOLYMYC, Figure 22).

Clones were screened for lysozyme binding activities as described in Examples 5 and 7 via the myc tag on the light chain variable domain, as this should permit the following kinds of V_x domains to be identified:

(1) those which bind to lysozyme in the absence of the VHLYS domain;

(2) those which associate with the heavy chain and make no contribution to binding of lysozyme; and

(3) those which associate with the heavy chain and also contribute to binding of lysozyme (either helping or hindering).

This would not identify those V_x domains which associated with the VHLYS domain and completely abolished its binding to lysozyme.

In a further experiment, the VHLYS domain was

replaced by the heavy chain variable domain VH3 which had been isolated from the repertoire (see Example 6), and then the V_x domains cloned into the vector. (Note that the VH3 domain has an internal SacI site and this was first removed to allow the cloning of the V_x repertoire as SacI-XhoI fragments.)

By screening the supernatant using the ELISA described in Example 6, bacterial supernatants will be identified which bind lysozyme.

Example 12

High expression of VH domains.

By screening several clones from a VH library derived from a mouse immunised with lysozyme via a Western blot, using the 9E10 antibody directed against the peptide tag, one clone was noted with very high levels of expression of the domain (estimated as 25 - 50 mg/l). The clone was sequenced to determine the nature of the sequence. The sequence proved to be closely related to that of the VHLYS domain, except with a few amino acid changes (Figure 23). The result was unexpected, and shows that a limited number of amino acid changes, perhaps even a single amino acid substitution, can cause greatly elevated levels of expression.

By making mutations of the high expressing domain at these residues, it was found that a single amino acid change in the VHLYS domain (Asn 35 to His) is sufficient to cause the domain to be expressed at high levels.

CONCLUSION

It can thus be seen that the present invention enables the cloning, amplification and expression of heavy and light chain variable domain encoding sequences in a much more simple manner than was previously possible. It also shows that isolated variable domains or such domains linked to effector molecules are unexpectedly useful.

It will be appreciated that the present invention has been described above by way of example only and that variations and modifications may be made by the skilled person without departing from the scope of the invention.

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Claims

1. A single domain ligand consisting of at least part of the variable domain of one chain of a molecule from the immunoglobulin (Ig) superfamily.
2. The ligand of claim 1, which consists of the variable domain of an Ig heavy chain.
3. The ligand of claim 1, which consists of the variable domain of an Ig chain with one or more point mutations from the natural sequence.
4. A receptor comprising a ligand of any one of claims 1 to 3 linked to one or more of an effector molecule, a prosthetic group, a label, a solid support or one or more other ligands having the same or different specificity.
5. The receptor of claim 4, comprising at least two ligands.
6. The receptor of claim 5, wherein the first ligand binds to a first epitope of an antigen and the second ligand binds to a second epitope.
7. The receptor of claim 6, which includes an effector molecule or label.
8. The receptor of any one of claims 5 to 7 which comprises a ligand and another protein mol-

ecule, produced by recombinant DNA technology as a fusion product.

9. The receptor of claim 8, wherein a linker peptide sequence is placed between the ligand and the other protein molecule.

10. A method of cloning a sequence (the target sequence) which encodes at least part of the variable domain of an Ig superfamily molecule, which method comprises:

(a) providing a sample of double stranded (ds) nucleic acid which contains the target sequence;

(b) denaturing the sample so as to separate the two strands;

(c) annealing to the sample a forward and a back oligonucleotide primer, the forward primer being specific for a sequence at or adjacent the 3' end of the sense strand of the target sequence, the back primer being specific for a sequence at or adjacent the 3' end of the antisense strand of the target sequence, under conditions which allow the primers to hybridise to the nucleic acid at or adjacent the target sequence;

(d) treating the annealed sample with a DNA polymerase enzyme in the presence of deoxynucleoside triphosphates under conditions which cause primer extension to take place; and

(e) denaturing the sample under conditions such that the extended primers become separated from the target sequence.

11. The method of claim 10, further including the step (f) of repeating steps (c) to (e) on the denatured mixture a plurality of times.

12. The method of claim 10 or claim 11, which is used to clone a complete variable domain from an Ig heavy chain.

13. The method of claim 10 or claim 11 which is used to produce a DNA sequence encoding a ligand according to any one of claims 1 to 3.

14. The method of any one of claims 10 to 13, wherein the forward and back primers are provided as single oligonucleotides.

15. The method of any one of claims 10 to 13, wherein the forward and back primers are each supplied as a mixture of closely related oligonucleotides.

16. The method of claim 14 or claim 15, wherein the primers which are used are species specific general primers.

17. The method of any one of claims 10 to 16, wherein the ds nucleic acid sequence is genomic DNA.

18. The method of any one of claims 10 to 17, wherein the ds nucleic acid is derived from a human.

19. The method of any one of claims 10 to 18, wherein the ds nucleic acid is derived from peripheral blood lymphocytes.

20. The method of any one of claims 10 to 18, wherein each primer includes a sequence encoding a restriction enzyme recognition site.

21. The method of claim 20, wherein the restriction enzyme recognition site is located in the sequence which is annealed to the ds nucleic acid.

22. The method of any one of claims 10 to 21, wherein the product ds cDNA is inserted into an expression vector and expressed alone.

23. The method of any one of claims 10 to 22, wherein the product ds cDNA is expressed in combination with a complementary variable domain.

24. The method of any one of claims 10 to 23, wherein the cloned ds cDNA is inserted into an expression vector already containing sequences encoding one or more constant domains to allow the vector to express Ig-type chains.

25. The method of any one of claims 10 to 24, wherein the cloned ds cDNA is inserted into an expression vector so that it can be expressed as a fusion protein.

26. The method of claim 10, wherein one or both of the primers comprises a mixture of oligonucleotides of hypervariable sequence, whereby a mixture of variable domain encoding sequences is produced.

27. A method of cloning a sequence (the target sequence) which encodes at least part of the variable domain of an Ig superfamily molecule, which method comprises:

(a) providing a sample of double stranded (ds) nucleic acid which contains the target sequence;

(b) denaturing the sample so as to separate the two strands;

(c) annealing to the sample a forward and a back oligonucleotide primer, the forward primer being specific for a sequence at or adjacent the 3' end of the sense strand of the target sequence, the back primer being specific for a sequence at or adjacent the 3' end of the antisense strand of the target sequence, under conditions which allow the primers to hybridise to the nucleic acid at or adjacent the target sequence;

(d) treating the annealed sample with a DNA polymerase enzyme in the presence of deoxynucleoside triphosphates under conditions which cause primer extension to take place;

(g) treating the sample of ds cDNA with traces of DNase in the presence of DNA polymerase I to allow nick translation of the DNA; and

(h) cloning the ds cDNA into a vector.

28. The method of claim 27, which further includes the steps of:

(i) digesting the DNA of recombinant plasmids to release DNA fragments containing genes encoding variable domains; and

(j) treating the fragments in a further set of

steps (c) to (h).

29. The method of either claim 27 or claim 28, wherein the fragments are separated from the vector and from other fragments of the incorrect size by gel electrophoresis.

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30. The method of any one of claims 27 to 29, wherein the product ds cDNA is cloned directly into an expression vector.

31. A species specific general oligonucleotide primer or mixture of such primers useful for cloning at least part of a variable domain encoding sequence from an animal of that species.

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32. A primer or mixture of primers according to claim 27, wherein each primer includes a restriction enzyme recognition site within the sequence which anneals to the coding part of the variable domain encoding sequence.

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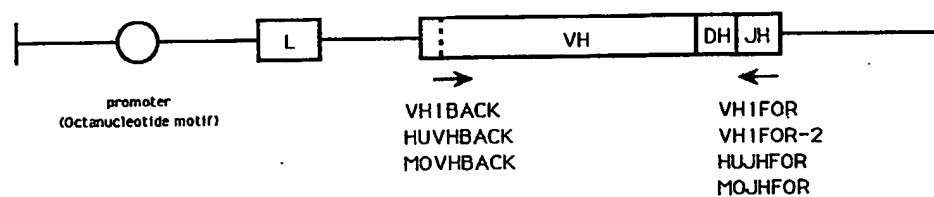
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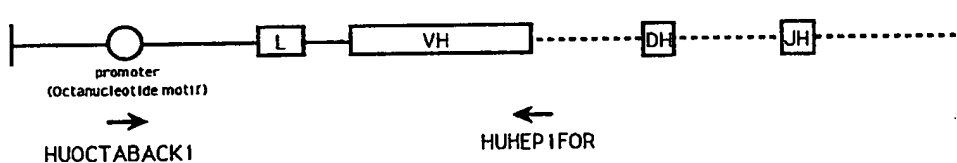
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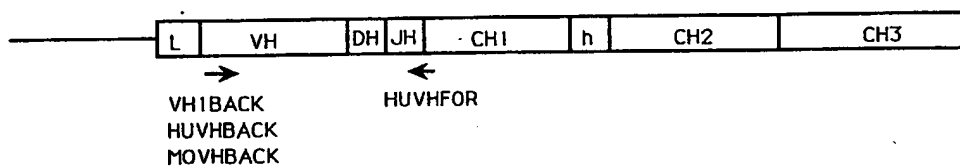
Rearranged heavy chain variable gene (DNA)



Unrearranged heavy chain variable gene (DNA)



Rearranged heavy chain variable gene (mRNA)



Rearranged light chain variable gene (DNA)

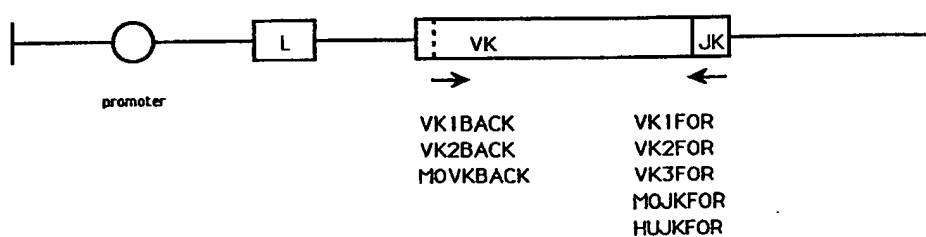


FIG. 1

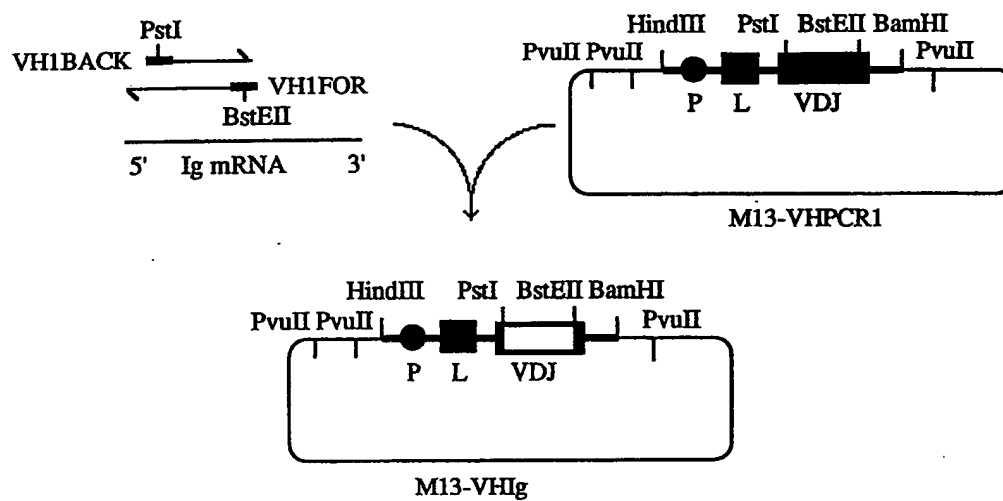


FIG. 2

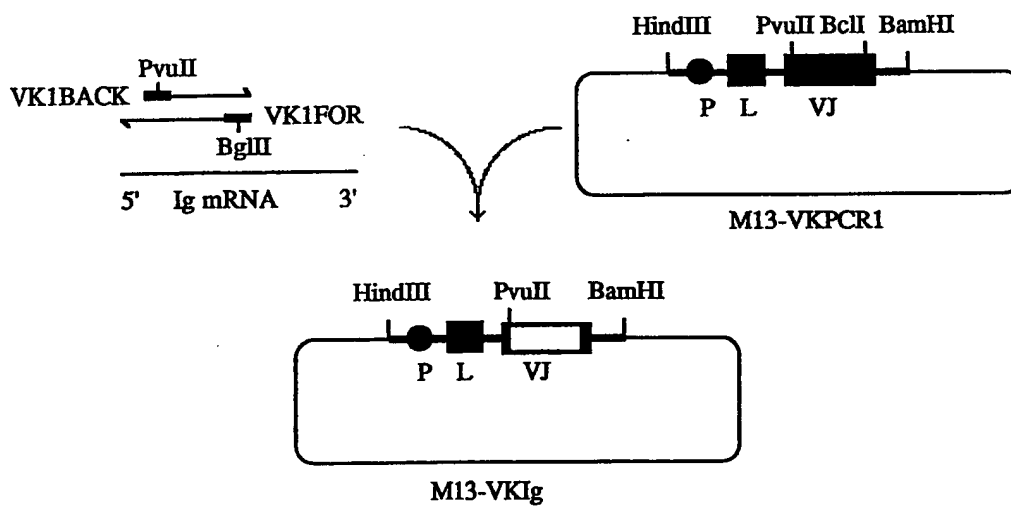


FIG. 4

M13 VHPCR1.Hind III^{a)}

|
 AAGCTTATGAATATGCAAATCCTCTGAATCTACATGGTAAATATAGGTTTGTCTATACCA
 10 20 30 40 50 60
 CAAACAGAAAACATGAGATCACAGTTCTCTCTACAGTTACTGAGCACACAGGACCTCAC
 70 80 90 100 110 120

M G W S C I I L F L V A T A T
 CATGGGATGGAGCTGTATCATCTCTTCTGGTAGCAACAGCTACAGGTAAGGGGCTCAC
 130 140 150 160 170 180

AGTAGCAGGCTTGAGGCTCTGGACATATATATGGGTGACAATGACATCCACTTTGCTTTTC
 190 200 210 220 230 240

PstI
 1 5 10
 G V H S Q V Q L Q E S G P G L V R P
 TCTCCACAGGTGTCCACTCCAGGTCCAACTGCAGGAGAGCGGTCCAGGTCTTGTGAGAC
 250 260 270 280 290 300

CDR1
 15 20 25 30
 S Q T L S L T C T V S G S T F S S Y W M
 CTAGCCAGACCTGAGCCTGACCTGCACCGTGTCTGGCAGCACTTCAGCAGCTACTGGA
 310 320 330 340 350 360

CDR2
 35 40 45 50
 H W V R Q P P G R G L E W I G R I D P N
 TGCAGTGGGTGAGACAGCCACTGGACGAGGTCTTGAGTGGATTGGAAGGATTGATCCTA
 370 380 390 400 410 420

55 60 65 70
 S G G T K Y N E K F K S R V T M L V D T
 ATAGTGGTGGTACTAAGTACAATGAGAAGTTCAAGAGCAGAGTGACAATGCTGGTAGACA
 430 440 450 460 470 480

75 80 85 90
 S K N Q F S L R L S S V T A A D T A V Y
 CCAGCAAGAACCAGTTTCAGCTGAGACTCAGCAGCGTGACAGCCGCGACACCGCGGTCT
 490 500 510 520 530 540

CDR3
 95 100 105 110
 Y C A R Y D Y Y G S S Y F D Y W G Q G T
 ATTATTGTGCAAGATACGATTACTACGGTAGTAGCTACTTTGACTACTGGGGCCAAGGGA
 550 560 570 580 590 600

BstEII
 115 | 120
 T V T V S S
 CCACGGTCACCGTCTCTCTCAGGTGAGTCTTACAACCTCTCTCTCTATTTCAGCTTAAAT
 610 620 630 640 650 660

AGATTTTACTGCATTTGTTGGGGGGGAAATGTGTGTATCTGAATTTTCAGGTTCATGAAGGA
 670 680 690 700 710 720

CTAGGGACACCTTGGGAGTCAGAAAGGGTCATTGGGAGCCCGGGCTGATGCAGACAGACA
 730 740 750 760 770 780

BamHI
 |
 TCCTCAGCTCCCAGACTTCATGGCCAGAGATTATAG
 790 800 810

FIG. 3

M13 V_H-PCR1

Hind III

AAGCTTATGAATATGCAAATCCTCTGAATCTACATGGTAAATATAGGTTTGTCTATACCA
 38 48 58 68 78 88

CAAACAGAAAACATGAGATCAGATTCTCTTACAGTTACTGAGCACACAGGACCTCAC
 98 108 118 128 138 148

M G W S C I I L F L V A T A T
 CATGGGATGGAGCTGTATCATCTCTTCTTGGTAGCAACAGCTACAGGTAAGGGGCTCAC
 158 168 178 188 198 208

AGTAGCAGGCTTGAGGCTCGACATATATATGGGTGACAATGACATCCACTTTGCCTTTC
 218 228 238 248 258 268

Pvu II

1 5 10
 G V H S D I Q L T Q S P S S L S A S
 TCTCCACAGGTGTCCACTCCGACATCCAGCTGACCCAGAGCCCAAGCAGCCTGAGCGCCA
 278 288 298 308 318 328

CDR1

15 20 25 30
 V G D R V T I T C R A S G N I H N Y L A
 GCGTGGGTGACAGAGTGACCATCACTGTAGAGCCAGCGGTAAACATCCACAACCTACCTGG
 338 348 358 368 378 388

CDR2

35 40 45 50
 W Y Q Q K P G K A P K L L I Y Y T T T L
 CTTGGTACCAGCAGAAGCCAGGTAAGGCTCCAAAGCTGCTGATCTACTACACCACACCC
 398 408 418 428 438 448

55 60 65 70
 A D G V P S R F S G S G S G T D F T F T
 TGGCTGACGGTGTGCCAAGCAGATTACGCGGTAGCGGTAGCGGTACCGACTTCACTTCA
 458 468 478 488 498 508

CDR3

75 80 85 90
 I S S L Q P E D I A T Y Y C Q H F W S T
 CCATCAGCAGCCTCCAGCCAGGACATGCCACCTACTACTGCCAGCACTTCTGGAGCA
 518 528 538 548 558 568

Bcl I (requires *dam*⁻ host)

95 100 105 108
 P R T F G Q G T K V V I K R
 CCCCAAGGAAGTTCCGCCAAGGGACCAAGGTGCTGATCAACGTCAGTAGAATTTAACT
 578 588 598 608 618 628

BamHI

TTGCTTCTCAGTTGGATCC
 638 648

FIG. 5

Sequence of MBr1 VK

FIG. 6

α -Lys 30

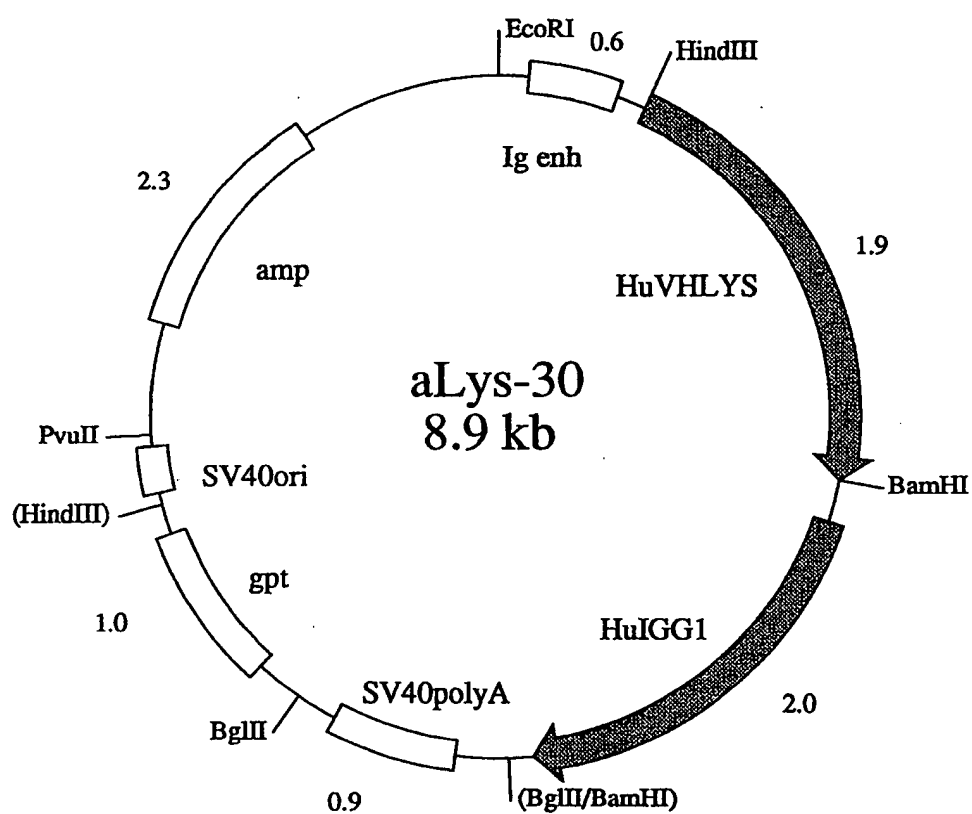


FIG. 7

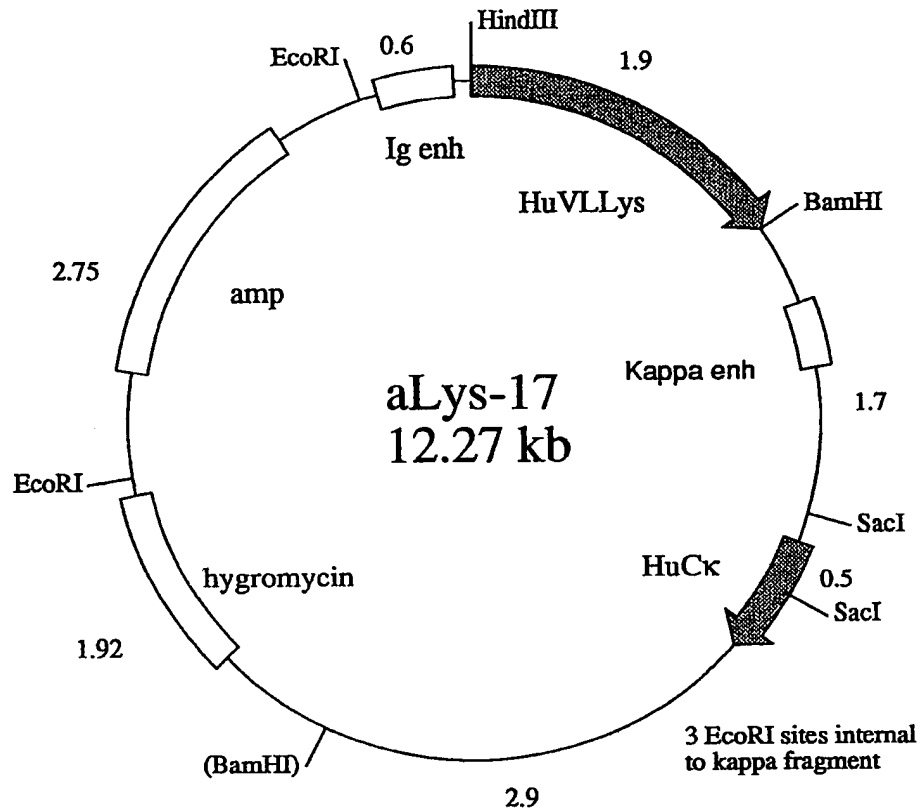
α -Lys 17

FIG. 8

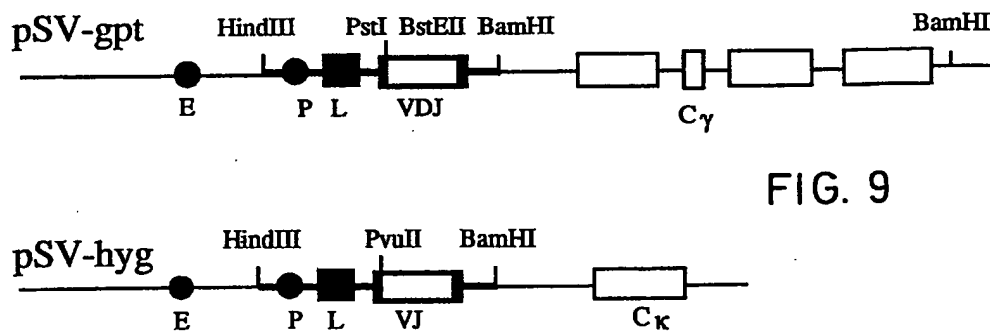


FIG. 9

	ER1	CDR 1	ER2	CDR 2
KABAT IA				
A07	PGLVKPSQSLSLTCSVTGYSIT	SGYYWN	WIRQFPGNKLEWMG	YISYDGSNNYNPSLKN
A09	PGLVKPSQSLSLTCSITGEPIT	SGYYWI	WIRQSPGKPLEWMG	YITHSGETFFYNPSLQS
E03	PGLVKPSQSLSLTCSVTGYSIT	SGYYWN	WIRQFPGNKLEWMG	YISYDGSNNYNPSLKN
G01	PGLVKPSQSLSLTCSVTGYSIT	SGYYWN	WIRQFPGNKLEWMG	YISYDGSNNYNPSLKN
KABAT IB				
A06	PVLVAPSQSLSLTCAVSDFSLT	NYGVL	WVRQPPGKGLEWLG	VIWAGGITNYSALMS
25G07	PGLVQPSQSLSLTCTVSGFSLT	SYGVH	WVRQSPGKGLEWLG	VIWSGGSTDYNAAFIS
B03	PGLVAPSQSLSLTCTVSGFSLT	SYGVD	WVRQPPGKGLEWLG	VIWGGGSTNYSALMS
G03	PGLVQPSQSLSLTCTVSGFSLT	SYGVH	WVRQSPGKGLEWLG	VIWSGGSTDYNAAFIS
H09	PVLVAPPSQSLSLTCTVSGFSLT	SYGVH	WVRQPPGKGLEWLG	VIWAGGSTNYSALMS
25C10	PGLVAPSQSLSLTCTVSGFSLT	SYAIS	WVRQPPGKGLEWLG	VIWTGGGTNYSALKS
A12	PGLVAPSQSLSLTCTVSGFSLT	SYAIS	WVRQPPGKGLEWLG	VIWTGGGTNYSALKS
A08	PGLVAPSQSLSLTCTVSGFSLT	SYGVH	WVRQPPGKGLEW**	*****GSTTYSALKS
25G08	PGLVAPSQSLSLTCTVSGFSLT	SYDVD	WVRQSPGKGLEWLG	VIWGGGSTNYSALKS
A03	PGLVQPSQSLSLTCTVSGFSLT	SYGVH	WVRQSPGKGLEWLG	VIWSGGSTDYNAAFIS
C07	PVLVAPSQSLSLTCTVSGFSLT	SYGVH	WVRQPPGKGLEWLG	VIWAGGSTNYSALMS
H04	PGLVAPSQSLSLTCTVSGFSLT	SYGVD	WVRQSPGKGLEWLG	VIWVGSTNYSALKS
KABAT IIA				
E04	PELVRPQSVKISCKGSGYTFT	DYAMH	WVKQSHAKSLEWIG	VISTYYGDASYNQKFKD
H07	PELVRPQSVKISCKGSGYTFT	DYAMH	WVKQSHAKSLEWIG	VISTYYGDASYNQKFKD
KABAT IIB				
A02	AELVMPGASVKLSCKASGYTFT	SYWMH	WVKQRPQGLEWIG	EIDPSDSYTNYNQKFKG
B04	AELVKPGASVKMSCKASGYTFT	SYWIT	WVKQRPQGLEWIG	DIYPGSGSTNYNEKFKS
C05	AELVKPGASVKLSCKASGYTFT	SYWMH	WVKQRPGRGLEWIG	RIDPNSGGTKYNEKFKS
C09	AELVKPGASVKLSCKASGYTFT	SYWMH	WVKQRPQGLEWIG	EINPSNGGTNYDEKFKS
D06	ASLVKPGASVKMSCKASGYTFT	SYWIT	WVKQRPQGLEWIG	DIYPGSGSTNYNEKFKS
D08	PELVKPGASVKLSCKASGYTFT	SYWMH	WVKQRPQGLEWIG	EINPSNGGTNYNEKFKS
E07	AELVRPGASVKLSCKASGYTFT	DYEMH	WVKQTPVHGLEWIG	AIDPETGGTAYNQKFKG
G08	PELVKPGASVKLSCKASGYTFT	DYYIN	WVKQRPQGLEWIG	WIYPGSGGTNYNEKFKG
G10	AELVKPGASVKVSKASGYTFT	SYWMH	WVKQRPQGLEWIG	RIHPSDSDTNYNEKFKG
25G09	AELVKPGASVKMSCKASGYTFT	TYPIE	WVKQNHGKSLEWIG	NFHPYNDTNYNEKFKG
F04	TELVRPGASVKLSCKASGYTFT	SYWMH	WVKQRPQGLEWIG	NINPSNGGTNYNQKFKG
H02	AELVKPGASVKLSCKASGYTFT	SYWMH	WVKQRPQGLEWIG	NIDPSDSETHYNOKFKD
H01	AELVMPGASVKLSCKASGYTFT	SYWMH	WVKQRPQGLEWIG	EIDPSDSYTNYN*KVCG
25C05	PELVKPGTSVKMSCKASGYTFT	NYWMK	WV*QRPQGLEWIG	QIFPASGSITYNEMHKO
B01	AELVKPGASVKMSCKASGYTFT	SYWIT	WVKQRPQGLEWIG	DIYPGSGSTNYNEKFKS
B05	AELVRPGSVKLSCKDSYFAM	RHAMH	WVKQRPBGLEWIG	SFTMYSDATEYSENFAG
B11	AELVKPGASVKMSCKASGYTFT	SYWIT	WVKQRPQGLEWIG	DIYPGSGSTNYNEKFKS
KABAT III A				
25G05	GGLVQAWGSLSLSCAASGFTFT	DYYMS	WVRQPPGKALEWLG	FIRNKANGYTTEYSASVRG
C10	GGLVQPGGSLSLSCAASGFTFT	DYYMN	WVRQPPGKALEWLA	LIRNKANGYTTEYSASVRG
B07	GGLVQPGGSLSLSCAASGFTFT	DYYMS	WVRQPPGKALEWLA	LIRNKANGYTTEYSASVRG
KABAT III B				
G05	GGLVKPGGSLKLSCAASGFTFS	DYGMH	WVRQAPKGLEWVA	YISSGSSTIYYADTVKG
B12	GGLVQPGESLKLSCESNEYFFP	SHDMS	WVR*****VA	AINSDGGSTIYPTIMER
D04	GGLVQPGGSLRLSCAASGFTFS	SYAMS	WVA*APGKGLEWVS	AISSGGSTIYADSVRG
D05	GGLVQPGGSLRLSCAASGFTFS	SYAMS	WVA*APGKGLEWVS	AISSGGSTIYADSVRG
F12	GGLVQPGESWKLSCVQQ****	*****	WVRQ*PEKRLLEVA	AINSDGGSTIYPTIMER
F06	GGLVQPGGSLRLSCAASGFTFS	SYAMS	WVA*APGKGLEWVS	AISSGGSTIYADSVRG
D02	GGLVQPGESLKLSCESNEYVIP	*HDMS	WVRQDSGE*LELVA	AINSDGGSTIYPTIMER
F09	GDLVKPGGSLKLSCAASGFTFS	SYGMS	WVRQTPDKRLEWVA	TISSGGSTIYPTDSVRG
KABAT III C				
E06	GGLVQPGGSMKLSCAASGFTFS	DAWMD	WVRQSPKGLEWVA	EIRNKANNHATYYAESVRG
KABAT V A				
C04	AELVKPGASVKLSCKASGYTFT	EYTIH	WVKQPSGQGLEWIG	WFYPGSGSIKYNEKFKD

FIG. 10a

FR 3

RISITRDTSKNQFFLKLNSTTTEDTATYYCAR
 PISITRETSKNQFFLQLNSTTTEDTAMYYCAG
 RISITRDTSKNQFFLQLNSTTTEDTATYYCAR
 RISITRDTSKNQFFLKLNSTTTEDTATYYCAR

CDR 3

EGNWDGFAY
 DRDKLGPWFAY
 DSSGSMDY
 VSSGYESMDY

RLSISKDTSKSQVFLKMNSLQDDTAVYYCAK
 RLSISKDNKSKSQVFFKMNSLQADDTAIYYCAR
 RLSISKDNKSKSQVFLKMNSLQDDTAMYYCAK
 RLSISKDNKSKSQVFFKMNSLQADDTAIYYCAR
 RLSISKDNKSKSQVFLKMNSLQDDTAMYYCAI
 RLSISKDNKSKSQVFLKMNSLQDDTARYYCAR
 RLSISKDNKSKSQVFLKMNSLQDDTARYYCAR
 RLSISKDNKSKSQVFLKMNSLQDDTAMYYCAR
 RLSISKDNKSKSQVFFKMNSLQADDTAIYYCAR
 RLSISKDNKSKSQVFLKMNSLQDDTAMYYCAK
 RLSISKDNKSKSQVFLKMNSLQDDTAMYYCAS

HGDSGGYFDY
 NDGY
 LGRGYAMDY
 KRQYDYGYYAMDY
 YDGSFFAY
 EGYYYFAY
 IYYDGSDDYYAMDY
 13 nt.
 21 nt.
 28 nt.
 37 nt.
 32 nt.

Ps.gene/Unproductive
 Unproductive
 Unproductive
 Unproductive
 Unproductive

KATMTVDKSSSTAYMELARLTSED SAVYYCAR
 KATMTVDKSSSTAYMELARLTSED SAVYYCAR

40 nt.
 22 nt.

Unproductive
 Unproductive

KATLTVDKSSSTAYMQLSSLTSED SAVYYCVR
 KATLTVDTSSTAYMQLSSLTSED SAVYYCAR
 KATLTVDKPSSTAYMQLSSLTSED SAVYYCAR
 KATLTVDKSSSTAYMQLSSLTSED SAVYYCTL
 KATLTVDTSSTAYMQLSSLTSED SAVYYCAR
 KATLTVDKSSSTAYMQLSSLTSED SAVYYCTI
 KATLTVDKSSSTAYMQLSSLTSED SAVYYCAR
 KATLTVDTSSTAYMQLSSLTSED SAVYYCAR
 KATLTVDKSSSTAYMQLSSLTSED SAVYYCAI
 KATLTVEKSSSTVYLELSRLTSD SAVYYCAR
 KATLTVDKSSSTAYMQLSSLTSED SAVYYCAK
 KATLTVDKSSSTAYMQLSSLTSED SAVYYCAR
 KATLTVDKSSSTAYMQLSSLTSED SAVYYCAP
 KAAWAVDTSSSTAYMQLSSLTSED TAVYFCL*
 KATLTVDKPSSTAYMQLSSLTSED SAVYYCAR
 KATLTANTSSSTAYMELSSLTSED SAVYYCAR
 KATLTVDTSSTSYMQLSSLTSED SAVYYCAR

RGLTYAMDY
 YYSNYFDY
 PNWDHYYYQMDV
 LYYAMDY
 SSGYDY
 GAARATNAY
 GGFAY
 SPMDY
 EVPGGFYATDY
 MDYGGSSLWFAY
 TTVAFDY
 KRQYSTYFDH
 TGTEFAY
 24 nt.
 9 nt.
 23 nt.
 15 nt.

Ps.gene
 Ps.gene/Unproductive
 Unproductive
 Unproductive
 Unproductive

RFTISRDNQSILYLQMNALRAEDSATYYCAR
 RFTISRDNQSILYLQMNALRAEDSATYYCAR
 RFTISRDNQSILYLQMNALRAEDSATYYCAR

YMIIGAMDY
 GYYYDGSYYAMDY
 23 nt.

Unproductive

RFTISRDNKNTLFLQMTSLRSED TAMYCAR
 RFIISRDNKNTLYLQMSLRAED TALIYYCAR
 RFTISRDNKNTLYLQMSLRAED TAVYYCAD
 RFTISRDNKNTLYLQMSLRAED TAVYYCAK
 RFIISRDNKNTLYLQMSLRAED TALIYYCAR
 RFTISRDNKNTLYLQMSLRAED TAVYYCAK
 RFIISRDNKNTLYLQMSLRAED TALIYYCAR
 RFTISRDNKNTLYLQMSLRAED TAVYYCAR

AKFHLYFDY
 REGVVESRLDGDV
 RGLHWFDP
 RNYGSSPFDY
 PPMMPY
 43 nt.
 28 nt.
 35 nt.

Ps.gene
 Ps.gene
 Ps.gene
 Ps.gene
 Ps.gene/Unproductive
 Ps.gene/Unproductive
 Unproductive

RFTISRDDSKSRVYLQMSLRAEDTGYYCTG

30 nt.

Unproductive

KATLTADKSSSTVYMELSRLTSED SAVYFCAR

HEDRDSSGYAMDY

FIG. 10b

<u>CDR 2</u>	<u>FRAMEWORK 3</u>	<u>CDR 3</u>
KABAT HUMAN VH1		
	STSTAYMELRSLRSED TAVVYCAR	GEGWDHFDY
HAQKFQG	RVTIRRHKSTSTAYMELSSLRSED TAVVYCAR	GSRYGYDCSGYYL
GIAQKFQG	RVTMTTRNTSISTATMELSSLRSED TAVVYCAR	LAHFGSPVDWFD
KABAT HUMAN VH2		
KHQLQPSLKS	RVTISVDTSKNQFSLKLSSVTAAD TAVVYCAR	GGVPAAIMDV
KS	RVTISVDTSKNQFSLKLSSVTAAD TAVVYCAR	MARYYDFWSGYSAYDY
SLKS	RLSISQDTSRNQFSLRLSSVTAAD TAVVYCAR	HRNWGSPVHFDY
	ESTSTAYMELSSLRSED TAVVYCAR	DSYGDYGGHY
KABAT HUMAN VH3		
ISYITSSSSYTNADSVKG	RFTISRDNKNSLYLQMNSLRADDTAVVYCAR	DGRFGTYSPSDY
SVKG	RFTISRDDSKSIAYLQVNSLKTEDTAVVYCTR	TIYYDSSGYPYW
YADSVKG	RFTISRDNKNSLFLQMSLRAEDTAVVYCAR	GIALDAFDI
YYADSVRD	RFTISRDNKNTLYLQMNSLRAEDTAVVYCAR	53 NT. UNPROD REARR
DSVKG	RFTISRDNKNSLYLQMNSLRDEDTAVVYCAR	DHSGTGGGSGSYF
VSAISGGSGSTYYADSVKG	RFTISRDNPKNTLYLQMNSLRSED TAVVYCAR	KDNLWFD
AVISYDGSNKYYADSVKG	RFTISRDNKNTLYLQMNSLRAEDTAVVYCAR	DLGGRGVVVVPAPGGRSIYYGMDV
GAVISYDGSNKYYADSVKG	RFTISRDNKNTLYLQMNSLRAEDTAVVYCAR	LEGIGTIYYGMDV
	AKNSLYLQMNSLRAEDTAVVYCVR	DDSSSWPKHFQ
QYAASVKG	RFTISRDDSKNSLYLQMNSLNTEDTAVVYCVR	SGVVPYLDY
KNOWN FAMILY		
	AVVYCAR	DPRIAARPDYYYMDV
	TAVVYCAR	GAEVVEPTARYYYGLNV

FIG. 11

	FR1	CDR1	FR2
	YTFT	SYGIS	WVTGPGWTRDLRWMG
GEKPGSSVKVCKASGYTFT		DYFMN	WMRQAPGQRLWWMG
QVQLQEI G PRTGEASETTL S LICAVSGDSIS		SGNW*I	WVRQPPGKGLEWIG
QVQLQESGPGLVK*SETLSLTCTVSGGSIS		SYIWS	WIRQPPGKGLEWIG
GYTFT		NYCMH	WVRQDHAQGLEWMG
QVQLQESGPGLVKpSETLSLYCAVSGDSIS		SGNW*I	WVRQPPGKGLEWIG
GPRLGEASETTL S LCTVSGGSIS		SSSYW	WIRQPPGKGLEWIG
QVQLQESGPGLVKpSETLSLTCTVSGGSIS		SYIWS	WIRQPPGKGLEWIG
LSLICAVSGGSIS		SGNW*I	WVRQPPGKGLEWIG
SETLSLTCAVYGGSF		GYIWS	WIRQPPGKGLEWIG
QVQLVQSGAEVKKPGASVKVCKASGYTFT		NYCMH	WVRQVLAQGLEWMG
SETLSLICAVSGDSIS		SGNW*I	WVRQPPGKGLEWIG
SRQQTGEASETTL S LCTVSGGSIS		SSSYWG	WIRQPPGKGLEWIG
CPLTCTVSGGSVSSGS		YIWS	WIRQPPGKGLEWIG
GLVKPSETLSLTCTVSGGSIS		SYIWS	WIGSPGKGLEWIG
SFETLSLICAVSGDSIS		SGNW*I	WVRQPPGKGLEWIG
QVQLVQSGAEVKKPGSSSVCKASGGTFS		SYAIS	WVRQAPGQGLEWMG
QVQLQQWGAGLLKPSSETLSLTCAVYGGSF		GYIWS	WIRQPPGKGLEWIG
QLQLQESGPGLVKPSSETLSLTCTVSGGSIS		SSSYWG	WIRQPPGKGLEWIG
GPGLVKPSQTL S LCTVSGGSIS		SGGYWS	WIRQNPCKGLEWIG

* indicates stop codon (unsure as sequence remains in frame)
 • sequence terminates due to internal restriction site
 lower case denotes frame shift

CDR2	FR3	CDR3
WISAYNGNTNYAQKLG	RVTMTDTSTSTAYMELSLRSDDTAVYYCAR	DTVSS
WINAGNGNTKY S QKLG	RVTITRDTASTAYMQLSSLRSED T AVYYCAR	DTVSS
EIHHS G STYYNPSLKS	RITMSVDT S KNQFY L KLSS•	
RIYTS G STNYNPSLKS	RVTISVDT S KNQFSLKLSSVTAADTAVYYCAR	DTVSS
LVCPSDG S TSYAQKFA	RVTITRDTSMSTAYMELSSLRSED T AMYYCAR	DTVSS
EIHHS G STYYNPSLKS	RITMSVDT S KNQFY L KLSS•	
EINHSGSTNYNPSLKS	RVTISVDT S KNQFSLKLSS•	
YIYSGSTNYNPSLKS	RVTISVDT S KNQFSLKLSS•	
EIHHS G STYYNPSLKS	RITMSVDT S KNQFY L KLSS•	
EINHSGSTNYNPSLKS	RVTISVDT S KNQFSLKLSSVTAADTAVYYCAR	DTVSS
LVCPSDG S TSYAQKFA	RVTITRDTSMSTAYMELSSLRSED T AMYYCAR	DTVSS
EIHHS G STYYNPSLKS	RITMSVDT S KNQFY L KLSS•	
SIYSGSTNYNPSLKS	RVTIPVDT S KNQFSLKLSS•	
YIYSGSTNYNPSLKS	RVTISVDT S KNQFSLKLSSVTAADTAVYYCAR	DTVSS
RIYTS G STNYNPSLKS	RVTMSVDT S KNQFSLKLSS•	
EIHHS G STYYNPSLKS	RITMSVDT S KNQFY L KLSS•	
RIIPILGIANYAQKFG	RVTITADKSTSTAYMELSSLRSED T AVYYCAR	DTVSS
EINHSGSTNYNPSLKS	RVTISVDT S KNQFSLKLSS•	
EINHSGSTNYNPSLKS	RVTISVDT S KNQFSLKLSS•	
YIYSGSTYYNPSLKS	RVTISVDT S KNQFSLKLSSVTAADTAVYYCAR	DTVSS

FIG. 12

pSW1

HindIII site AAGCTT

```

                                M K Y L L P T A A
GCATGCAAATTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
   10       20       30       40       50       60

A G L L L L A A Q P A M A Q V Q L Q E S
GCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGGCCAGGTGCAGCTGCAGGAGTCA
   70       80       90      100      110      120

G P G L V A P S Q S L S I T C T V S G F
GGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCAGGGTTC
  130      140      150      160      170      180

S L T G Y G V N W V R Q P P G K G L E W
TCATTAACCGGCTATGGTGTAACCTGGGTTCGCCAGCCTCCAGGAAAGGGTCTGGAGTGG
  190      200      210      220      230      240

L G M I W G D G N T D Y N S A L K S R L
CTGGGAATGATTGGGGTGATGGAACACAGACTATAATTCAGCTCTCAAATCCAGACTG
  250      260      270      280      290      300

S I S K D N S K S Q V F L K M N S L H T
AGCATCAGCAAGGACAACCTCCAAGAGCCAAGTTTTCTTAAAAATGAACAGTCTGCACACT
  310      320      330      340      350      360

D D T A R Y Y C A R E R D Y R L D Y W G
GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGATTATAGGCTTGACTACTGGGGC
  370      380      390      400      410      420

Q G T T V T V S S                                SmaI
CAAGGCACCAACGGTCACCGTCTCCTCATAATAAGAGCTATCCCGGGCTAAGCTCGAATTC
  430      440      450      460      470      480

```

FIG. 13

pSW2

HindIII AAGCTT

```

                                M K Y L L P T A A
GCATGCAAATTCATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
  10      20      30      40      50      60

  A G L L L L A A Q P A M A Q V Q L Q E S
GCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGGCCAGGTGCAGCTGCAGGAGTCA
  70      80      90     100     110     120

  G P G L V A P S Q S L S I T C T V S G F
GGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCAGGGTTC
 130     140     150     160     170     180

  S L T G Y G V N W V R Q P P G K G L E W
TCATTAACCGGCTATGGTGTAAACTGGGTTCCGCCAGCCTCCAGGAAAGGGTCTGGAGTGG
 190     200     210     220     230     240

  L G M I W G D G N T D Y N S A L K S R L
CTGGGAATGATTGGGGTGATGGAAACACAGACTATAATTAGCTCTCAAATCCAGACTG
 250     260     270     280     290     300

  S I S K D N S K S Q V F L K M N S L H T
AGCATCAGCAAGGACAACCTCAAGAGCCAAGTTTTCTTAAAAATGAACAGTCTGCACACT
 310     320     330     340     350     360

  D D T A R Y Y C A R E R D Y R L D Y W G
GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGATTATAGGCTTGACTACTGGGGC
 370     380     390     400     410     420

  Q G T T V T V S S
CAAGGCACCACGGTCACCGTCTCCTCATAATAAGAGCTCGAATTCGCCAAGCTTGCATGC
 430     440     450     460     470     480

                                M K Y L L P T A A A G
AAATTCATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCCGCTGGA
 490     500     510     520     530     540

  L L L L A A Q P A M A D I V L T Q S P A
TTGTTATTACTCGCTGCCCAACCAGCGATGGCCGACATCGTCCTGACTCAGTCTCCAGCC
 550     560     570     580     590     600

  S L S A S V G E T V T I T C R A S G N I
TCCCTTTCTGCGTCTGTGGGAGAACTGTCACCATCACATGTGAGCAAGTGGGAATATT
 610     620     630     640     650     660

  H N Y L A W Y Q Q K Q G K S P Q L L V Y
CACAATTATTTAGCATGGTATCAGCAGAAACAGGGAAATCTCCTCAGTCTCCTGGTCTAT
 670     680     690     700     710     720

```

FIG. 14a

Y T T T L A D G V P S R F S G S G S G T
TATACAACAACCTTAGCAGATGGTGTGCCATCAAGGTCAGTGGCAGTGGATCAGGAACA
730 740 750 760 770 780

Q Y S L K I N S L Q P E D F G S Y Y C Q
CAATATTCTCTCAAGATCAACAGCCTGCAACCTGAAGATTTTGGGAGTTATTACTGTCAA
790 800 810 820 830 840

H F W S T P R T F G G G T K L E I K R
CATTTTGGAGTACTCCTCGGACGTTGCGGTGGAGGCACCAAGCTGGAATCAAACGGTAA
850 860 870 880 890 900

TAAGAGCTCGAATTC
910

FIG. 14 b

pSWLHPOLYMYC

HindIII site AAGCTT

M K Y L L P T A A
GCATGCAAAATTCATTTCAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
10 20 30 40 50 60

A G L L L L A A Q P A M A Q V Q L Q
GCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGCCCCAGGTGCAGCTGCAG
70 80 90 100 110 PstI

Polylinker

TCTAGA GTCGAC CTCGAG
XbaI SalI XhoI

MYC PEPTIDE

V T V S S E O K L I S E E D L N * *
GGTCACCGTCTCCTCAGAACAAAACTCATCTCAGAAGAGGATCTGAATTAATAA
BstEII

GGGCTAAGCTCGAATTC

FIG. 15

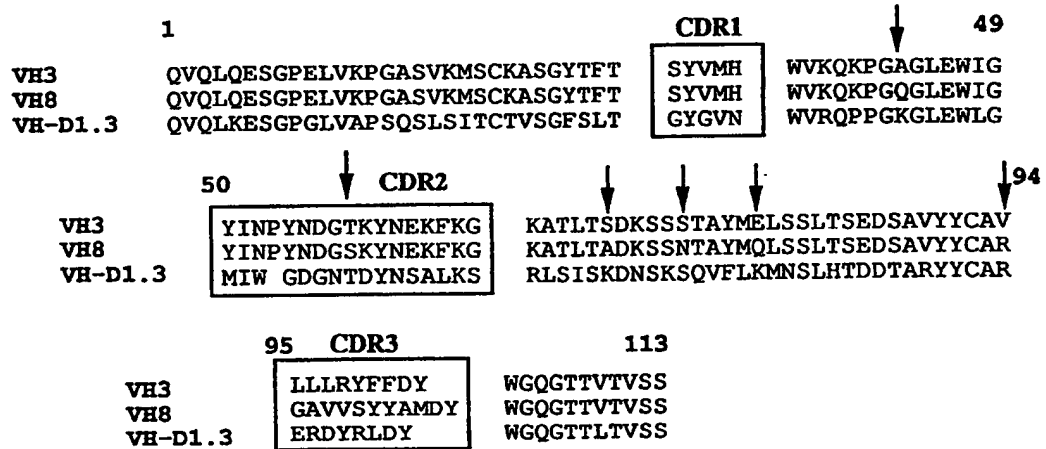


FIG. 16

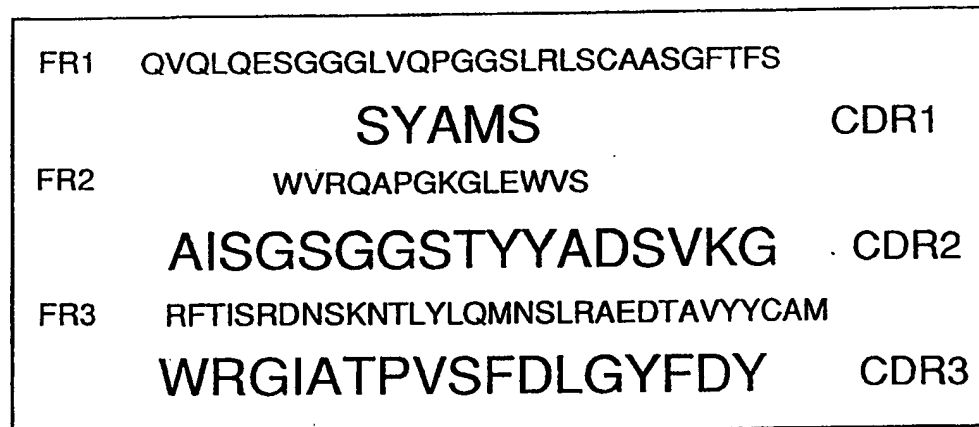


FIG. 17

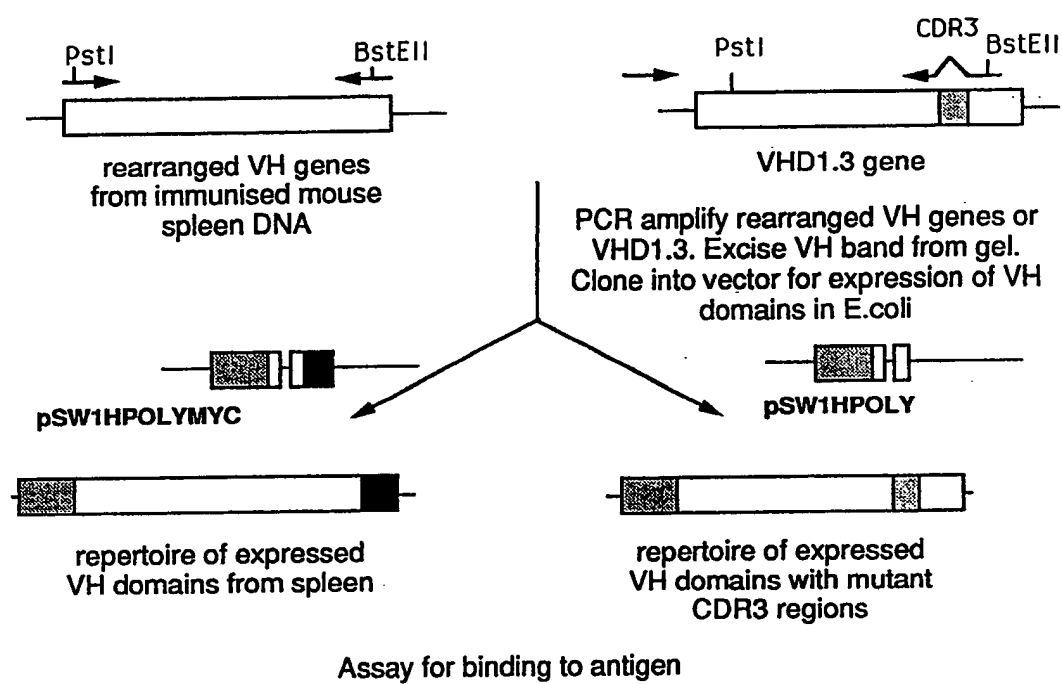


FIG. 18

pSW2HPOLY

HindIII AAGCTT

M K Y L L P T A A
 GCATGCAAATTCATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
 10 20 30 40 50 60

A G L L L L A A Q P A M A Q V Q L Q
 GCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGGCCAGGTGCAGCTGCAG
 70 80 90 100 110 PstI

TCTAGA GTCGAC CTCGAG
 XbaI SalI XhoI

V T V S S
 GGTCAACCGTCTCCTCATAATAAGAGCTCGAATTCGCCAAGCTTGCATGC
 BstEII 430 440 450 460 470 480

M K Y L L P T A A A G
 AAATTCATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCGCTGGA
 490 500 510 520 530 540

L L L L A A Q P A M A D I V L T Q S P A
 TTGTTATTACTCGCTGCCCAACCAGCGATGGCCGACATCGTCTGACTCAGTCTCCAGCC
 550 560 570 580 590 600

S L S A S V G E T V T I T C R A S G N I
 TCCCTTTCTGCGTCTGTGGGAGAACTGTCACCATCACATGTCGAGCAAGTGGGAATATT
 610 620 630 640 650 660

H N Y L A W Y Q Q K Q G K S P Q L L V Y
 CACAATTATTTAGCATGGTATCAGCAGAAACAGGGAAAATCTCCTCAGCTCCTGGTCTAT
 670 680 690 700 710 720

Y T T T L A D G V P S R F S G S G S G T
 TATACAACAACCTTAGCAGATGGTGTGCCATCAAGGTTCACTGGCAGTGGATCAGGAACA
 730 740 750 760 770 780

Q Y S L K I N S L Q P E D F G S Y Y C Q
 CAATATTCTCTCAAGATCAACAGCCTGCAACCTGAAGATTTGGGAGTTATTACTGTCAA
 790 800 810 820 830 840

H F W S T P R T F G G G T K L E I K R
 CATTTTGGAGTACTCCTCGGACGTTTCGGTGGAGGCACCAAGCTGGAAATCAAACGGTAA
 850 860 870 880 890 900

TAAGAGCTCGAATTC
 910

FIG. 19

M K Y L L P T
 AAGCTTGCATGCAAATTCATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACG
 10 20 30 40 50 60
 A A A G L L L L A A Q P A M A Q V Q L Q
 GCAGCCGCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGGCCCAGGTGCAGCTCAG
 70 80 90 100 110 120
 E S G P G L V A P S Q S L S I T C T V S
 GAGTCAGGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCA
 130 140 150 160 170 180
 G F S L T G Y G V N W V R Q P P G K G L
 GGGTTCTCATTAAACCGGCTATGGTGTAAGTGGGTTCCGCCAGCCTCCAGGAAAGGGTCTG
 190 200 210 220 230 240
 E W L G M I W G D G N T D Y N S A L K S
 GAGTGGCTGGGAATGATTTGGGGTGATGGAAACACAGACTATAATTCAGCTCTCAAATCC
 250 260 270 280 290 300
 R L S I S K D N S K S Q V F L K M N S L
 AGACTGAGCATCAGCAAGGACAACCTCCAAGAGCCAAGTTTCTTAAAAATGAACAGTCTG
 310 320 330 340 350 360
 H T D D T A R Y Y C A R E R D Y R L D Y
 CACACTGATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGATTATAGGCTTGACTAC
 370 380 390 400 410 420
 W G Q G T T V T V S S G G G A P A A A P
 TGGGGCCAAGGCACACCGGTCAACCGTCTCCTCAGGTGGTGGTGTCCAGCAGCTGCACCT
 430 440 450 460 470 480
 A G G G Q V Q L K E S G P G L V A P S Q
 GCTGGAGGAGGACAGGTGCAGCTGAAGGAGTCAGGACCTGGCCTGGTGGCGCCCTCACAG
 490 500 510 520 530 540
 S L S I T C T V S G F S L T G Y G V N W
 AGCCTGTCCATCACATGCACCGTCTCAGGGTTCTCATTAAACCGGCTATGGTGTAAGTGG
 550 560 570 580 590 600
 V R Q P P G K G L E W L G M I W G D G N
 GTTCGCCAGCCTCCAGGAAAGGGTCTGGAGTGGCTGGGAATGATTTGGGGTGATGGAAAC
 610 620 630 640 650 660
 T D Y N S A L K S R L S I S K D N S K S
 ACAGACTATAATTCAGCTCTCAAATCCAGACTGAGCATCAGCAAGGACAACCTCCAAGAGC
 670 680 690 700 710 720
 Q V F L K M N S L H T D D T A R Y Y C A
 CAAGTTTTCTTAAAAATGAACAGTCTGCACACTGATGACACAGCCAGGTACTACTGTGCC
 730 740 750 760 770 780
 R E R D Y R L D Y W G Q G T T V T V S S
 AGAGAGAGAGATTATAGGCTTGACTACTGGGGCCAAGGCACCAAGGTCAACCGTCTCCTCA
 790 800 810 820 830 840
 * *
 TAATAAGAGCTC
 850

FIG. 20

M K Y L L P T A A
 GCATGCAAATTCATTTCAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
 10 20 30 40 50 60
 A G L L L L A A Q P A M A Q V Q L Q E S
 GCTGGATTGTTATTACTCGCTGCCAACCAGCGATGGCCCAGGTGCAGCTGCAGGAGTCA
 70 80 90 100 110 120
 G P G L V A P S Q S L S I T C T V S G F
 GGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCAGGGTTC
 130 140 150 160 170 180
 S L T G Y G V N W V R Q P P G K G L E W
 TCATTAACCGGCTATGGTGTAACCTGGGTTCGCCAGCCTCCAGGAAAGGGTCTGGAGTGG
 190 200 210 220 230 240
 L G M I W G D G N T D Y N S A L K S R L
 CTGGGAATGATTGGGGTGATGGAAACACAGACTATAATTCAGCTCTCAAATCCAGACTG
 250 260 270 280 290 300
 S I S K D N S K S Q V F L K M N S L H T
 AGCATCAGCAAGGACAACCTCCAAGAGCCAAGTTTCTTAAAAATGAACAGTCTGCACACT
 310 320 330 340 350 360
 D D T A R Y Y C A R E R D Y R L D Y W G
 GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGATTATAGGCTTGACTACTGGGGC
 370 380 390 400 410 420
 Q G T T V T V S S R T P E M P V L E N R
 CAAGGCACCACGGTCACCGTCTCCTCACGGACACCAGAAATGCCTGTTCTGGAAAACCGG
 430 440 450 460 470 480
 A A Q G D I T A P G G A R R L T G D Q T
 GCTGCTCAGGGCGATATTACTGCACCCGGCGGTGCTCGCCGTTTAAACGGGTGATCAGACT
 490 500 510 520 530 540
 A A L R D S L S D K P A K N I I L L I G
 GCCGCTCTGCGTGATTCTCTTAGCGATAAACCTGCAAAAAATATTATTTTCTGATTGGC
 550 560 570 580 590 600
 D G M G D S E I T A A R N Y A E G A G G
 GATGGGATGGGGGACTCGGAAATTACTGCCGCACGTAATTATGCCGAAGGTGCGGGCGGC
 610 620 630 640 650 660
 F F K G I D A L P L T G Q Y T H Y A L N
 TTTTAAAGGTATAGATGCCTTACCGCTTACCGGGCAATACACTCACTATGCGCTGAAT
 670 680 690 700 710 720
 K K T G K P D Y V T D S A A S A T A W S
 AAAAAACCGGCAACCGGACTACGTACCGACTCGGCTGCATCAGCAACCGCTGGTCA
 730 740 750 760 770 780

FIG. 21a

T G V K T Y N G A L G V D I H E K D H P
 ACCGGTGTCAAACCTATAACGGCGCGCTGGGCGTCGATATTCAGAAAAAGATCACCCA
 790 800 810 820 830 840

T I L E M A K A A G L A T G N V S T A E
 ACGATTCTGGAAATGGCAAAAGCCGCAGGTCTGGCGACCGGTAACGTTTCTACCGCAGAG
 850 860 870 880 890 900

L Q D A T P A A L V A H V T S R K C Y G
 TTGCAGGATGCCACGCCCGCTGCGCTGGTGGCACATGTGACCTCGCGCAATGCTACGGT
 910 920 930 940 950 960

P S A T S E K C P G N A L E K G G K G S
 CCGAGCGCGACCACTGAAAAATGTCCGGGTAACGCTCTGGAAAAAGCGGAAAAGGATCG
 970 980 990 1000 1010 1020

I T E Q L L N A R A D V T L G G G A K T
 ATTACCGAACAGCTGCTTAACGCTCGTGCCGACGTTACGCTTGCGGGCGGCGCAAAACC
 1030 1040 1050 1060 1070 1080

F A E T A T A G E W Q G K T L R E Q A Q
 TTTGCTGAAACGGCAACCGCTGGTGAATGGCAGGAAAAACGCTGCGTGAACAGGCACAG
 1090 1100 1110 1120 1130 1140

A R G Y Q L V S D A A S L N S V T E A N
 GCGCGTGGTTATCAGTTGGTGAGCGATGCTGCCTCACTGAATTCGGTGACGGAAGCGAAT
 1150 1160 1170 1180 1190 1200

Q Q K P L L G L F A D G N M P V R W L G
 CAGCAAAAACCCCTGCTTGGCCTGTTGCTGACGGCAATATGCCAGTGCGCTGGCTAGGA
 1210 1220 1230 1240 1250 1260

P K A T Y H G N I D K P A V T C T P N P
 CCGAAAGCAACGTACCATGGCAATATCGATAAGCCCGCAGTCACCTGTACGCCAAATCCG
 1270 1280 1290 1300 1310 1320

Q R N D S V P T L A Q M T D K A I E L L
 CAACGTAATGACAGTGTACCAACCCCTGGCGCAGATGACCGACAAAGCCATTGAATTGTTG
 1330 1340 1350 1360 1370 1380

S K N E K G F F L Q V E G A S I D K Q D
 AGTAAAAATGAGAAAGGCTTTTTCTGCAAGTTGAAGGTGCGTCAATCGATAAACAGGAT
 1390 1400 1410 1420 1430 1440

H A A N P C G Q I G E T V D L D E A V Q
 CATGCTGCGAATCCTTGTGGGCAAATTGGCGGAGACGGTCGATCTCGATGAAGCCGTACAA
 1450 1460 1470 1480 1490 1500

R A L E F A K K E G N T L V I V T A D H
 CGGGCGCTGGAATTCGCTAAAAAGGAGGGTAACACGCTGGTCATAGTCACCGCTGATCAC
 1510 1520 1530 1540 1550 1560

FIG. 21b

A H A S Q I V A P D T K A P G L T Q A L
G C C C A G C C C A G C C A G A T T G T T G C G C C G G A T A C C A A G C T C C G G G C C T C A C C C A G G C G C T A
1570 1580 1590 1600 1610 1620

N T K D G A V M V M S Y G N S E E D S Q
A A T A C C A A A G A T G G C G C A G T G A T G G T G A T G A G T T A C G G G A A C T C C G A A G A G G A T T C A C A A
1630 1640 1650 1660 1670 1680

E H T G S Q L R I A A Y G P H A A N V V
G A A C A T A C C G G C A G T C A G T T G C G T A T T G C G G C G T A T G G C C C G C A T G C C G C C A A T G T T G T T
1690 1700 1710 1720 1730 1740

G L T D Q T D L F Y T M K A A L G L K *
G G A C T G A C C G A C C A G A C C G A T C T C T T C T A C A C C A T G A A A G C C G C T C T G G G G C T G A A A T A A
1750 1760 1770 1780 1790 1800

A A C C G C G C C C G G G A G T G A A T T T C G C T G C C G G G T G G T T T T T T G C T G T T A G C
1810 1820 1830 1840 1850

FIG. 21c

M K Y L L P T A A
 GCATGCAAAATTTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
 10 20 30 40 50 60
 A G L L L L A A Q P A M A Q V Q L Q E S
 GCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGGCCCAGGTGCAGCTGCAGGAGTCA
 70 80 90 100 110 120
 G P G L V A P S Q S L S I T C T V S G F
 GGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCAGGGTTC
 130 140 150 160 170 180
 S L T G Y G V N W V R Q P P G K G L E W
 TCATTAACCGGCTATGGTGTAAGTGGGTTGCCAGCCTCCAGGAAAGGGTCTGGAGTGG
 190 200 210 220 230 240
 L G M I W G D G N T D Y N S A L K S R L
 CTGGGAATGATTGGGGTGATGGAAACACAGACTATAATTCAGCTCTCAAATCCAGACTG
 250 260 270 280 290 300
 S I S K D N S K S Q V F L K M N S L H T
 AGCATCAGCAAGGACAACTCCAAGAGCCAAGTTTCTTAAAAATGAACAGTCTGCACACT
 310 320 330 340 350 360
 D D T A R Y Y C A R E R D Y R L D Y W G
 GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGATTATAGGCTTGACTACTGGGGC
 370 380 390 400 410 420
 Q G T T V T V S S * *
 CAAGGCACCACGGTCACCGTCTCCTCATAATAAGAGCTATCCCGGGAGCTTGCAATGCAAA
 430 440 450 460 470 480
 M K Y L L P T A A A G L
 TTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCCGCTGGATTG
 490 500 510 520 530 540
 L L L A A Q P A M A D I E L V D L E I K
 TTATTACTCGCTGCCCAACCAGCGATGGCCGACATCGAGCTCGTCGACCTCGAGATCAAA
 550 560 570 580 590 600
 R E Q K L I S E E D L N * *
 CGGGAACAAAACTCATCTCAGAAGAGGATCTGAATTAATAATGATCAAACGGTAATAAG
 610 620 630 640 650 660
 GATCCAGCTCGAATTC
 670

FIG. 22

Q V Q L Q E S G P G L V Q P S Q S L S I
 CAGGTGCAGCTGCAGGAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATC
 10 20 30 40 50 60

T C T V S G F S L T S Y G V H W V R Q S
 ACCTGCACAGTCTCTGGTTTCTCATTAAGCTATGGTGTACACTGGGTTGCGCCAGTCT
 70 80 90 100 110 120

P G K G L E W L G M I W G D G N T D Y N
 CCAGGAAAGGGTCTGGAGTGGCTGGGAATGATTTGGGGTGATGGAAACACAGACTATAAT
 130 140 150 160 170 180

S A L K S R L S I S K D N S K S Q V F L
 TCAGCTCTCAAATCCAGACTGAGCATCAGCAAGGACAACCTCCAGAGCCAAGTTTCTTA
 190 200 210 220 230 240

K M N S L H T D D T A R Y Y C A R E R D
 AAAATGAACAGTCTGCACACTGATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAT
 250 260 270 280 290 300

Y R L D Y W G Q G T T V T V S S
 TATAGGCTTGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
 310 320 330 340

FIG. 23